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Sequence 1114, Ap. Sequence 115, Ap. Sequence 150, Appli Sequence 150, Appli Sequence 170, Appl Sequence 170, Appl Sequence 170, Appl Sequence 176, Appl Sequence 189, Appl Sequence 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 484, App
Sequence 427, App
Sequence 427, App
Sequence 427, App
Sequence 427, App
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Sequence 473, 1
Sequence 473, 1
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Sequence 480
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Sequence 1
Sequence 3
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APPLICANT: MCNabb, Andria
APPLICANT: McNabb, Andria
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Read, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT RAPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 500
LENGTH: 577
         US-10-007-700-427
US-10-117-982-427
US-10-313-986-427
US-10-313-986-486
US-09-873-637-21
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US-10-313-986-473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 500, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
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ORGANISM: Homo
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Command line parameters:

-MODEL=frame+ n2p,model -DEV=xlp
-Q=/cgn2 1/USFD-gpcol p/US09270437/runat 13072004_121958_10114/app_query.fasta_1.1863
-Q=/cgn2 1/USFD-gpcol p/US09270437/runat 13072004_121958_10114/app_query.fasta_1.1863
-DB=Published_Applications_AA -QFMT=fasta_ -SUFFIX=rapb -MINMATCH=0.1
-LOPCH=0 -LOOPCH=0 -NUNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human46.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=60 -XGAPEXT=60
-LONGLOG -DEV TIMEOUT=17 -YGAPOP=60 -YGAPEXT=60 -DBLOREXT=7
                                                                                                                                              July 13, 2004, 12:34:44 ; Search time 88 Seconds (without alignments) 12108.099 Million cell updates/sec
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560
1 agggacgctgccgcaccgcc.....atttccttcaggttttaaaa 1708
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'(gn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
'(gn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
'(gn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
'(gn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
'(gn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
'(gn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
'(gn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
'(gn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
'(gn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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'(gn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                  protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1279676 segs, 311918243 residues
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Ygapop 60.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Maximum DB :
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ATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATTTATGGCAAACTTCAAGGCTCAGGGAAGAATTTTTGGCAAACTTCAAGGCTCAGGGAAGAATTTTTTTT	1172 AATTGACGCGGCTGGTGGTACTACCAAGAGACCAGACCTGATGAGAACCACCGGTGATGAGAACCACCGGTGATGAGAACCACCGGTGATGAGAACCACGGGTGATGAGAACCACGGGTGAAGAGAGAG	Qy         1292 GACATCCTGGCCCAGGTTAAGCAGCAGCAGAGTAACCAGGCCCAGGCCT 1351	RESULT 2 US-09-764-864-1114 US-09-764-864-1114 US-09-764-864-1114 US-09-764-864-1114 US-09-764-864-1114 US-09-764-864-1114 US-09-764-864-1114 US-09-764-864-1114 US-09-764-1114 US-09-764-114 US-09-	CURRENT APPLICATION NUMBER: US/09/764,864  CURRENT FILING DATE: 2001-01-17  Prior application data removed - consult PALM or file wrapper  NUMBER OF SEQ ID NOS: 1792  SOFTWARE: Patentin Ver. 2.0  SEQ ID NO 1114  LENGTH: 261  TYPE: PRT  CONTAINS HOME SENIOR	US-09-764-864-1114  Alignment Scores: 1.26e-197 Length: 261  Pred. No.: 216.00 Matches: 216  Percent Similarity: 100.00% Conservative: 0  Best Local Similarity: 100.00% Mismatches: 0  Query Match: 38.57% Indels: 0  DB:	US-09-270-437D-5 (1-1708) x US-09-764-864-1114 (1-261)  QY 713 TCTCACCTGATCCCTGGCCTGAACCTGGCTGCTGTAGGTCTTTTCCCAGGTTCATCCAGG 772	Oy 773 GCAGTCCCGCCGCCTCCCAGCGCGTTACTGGGGCTGCTCCCTATAGCTGGGGGGGTGCTCCTTTATGCAG 832		OY 893 GGCAAGAAGGGCACATCAAACAGCTCTCCCGGTTTGCCAGGGCCTCCATCAAGATT 952
Pred. No.:  Score:  Score:  Score:  261.00  Matches:  441  Percent Similarity:  99.55\$  Mismatches:  0  Ouery Match:  15  Mismatches:  16  Mismatches:  16  Mismatches:  17  Mismatches:  18  Mismatches:  19  Mismatches:  10  Mis	Qy         98 CCCGATGAGCAGATAGCACAGGGACCTGAGAATGGCGCGAGGGGGCTTTGGCTCTCGG         157           Db         155 ProAspGluGlnIleAlaGlnGlyProGluAsnGlyArgArgGlyGlyPheGlySerArg         174           Qy         158 GGTCAGCCCCGCCCAGGCTCACTGGCGGGGGGGGCCCCAGCCAG	GGCTCC         rgleuL GCAACA         rgAsnI	മവമെ	Qy         458 GACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAAG 517           Db         275 AspGluValProLeuLysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGlyLys 294           Qy         518 GAAGGACGGAACCTGAAGAAGGTAGAGTACCGACACAAAATCACCATCTCCTCG 577           Db         295 GluGlyArgAsnLeuLysLysValGluGinAspThrGluThrLysIleThrIleSerSer 314	Oy 578 TIGCAAGACCTTACCCTTACAACCTGAGACCATCACTGTGAAGGGGCCATCGAG 637	uGlns CAGCG       rSerA	OY 812 CCCTATAGGTCCTTTATGGAGGCTCCCGAGGAGGAGGAGGTGGTTTATCCCGGC 871 	Cy 872 CAGGCAGTGGCCCATCATCGGCAAGAAGGGCAGCACATCAAACAGCTCTCCCGGTTT 931	OY 932 GCCAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTATGGTT 991

514

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naturally occurring L-amino acids
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                          AlaAspGluValProLeuLysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGly
                                                                                                           TCGTTGCAAGACCTTACCTTTACAACCCTGAGGACCATCACTGTGAAGGGGCCCATC
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Fatent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PT223
CURRENT APPLICATION UNMERS: US/09/764,864
CURRENT FILING DATE: 2001-01-7
Frior application data removed - consult PALM or
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1532
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ORGANISM: Homo sapiens
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NAME/KEY: SITE

LOCATION: (127)

OTHER INPORMATION: Xe

NAME/KEY: SITE

LOCATION: (134)

OTHER INPORMATION: Xe

US-09-764-864-1532
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Best Local Similarity:
Query Match:
DB:
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US-09-764-864-1532
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US-09-873-637-2
US-09-873-637-2
; Pacture 2, Application US/09873637
; Patent No. US20020061543A1
; GENERAL INFORMATION:
; APPLICANT: ROSS, JOHEFEY
; TITLE OF INVENITON: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873,637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 577
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GCACCACCGGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAG
                                                                                  GCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGT
                                                                                                                                                                 CCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGG
                                                                                                                                                                                                                                                                            146 AlaGlnPheLysAlaGlnGlyArgIleTyrGlyLysLeuLysGluGluAsnPhePheGly
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; ORGANISM: Mus musculus
US-09-873-637-2
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Pred. No.:
Score:
Percent Similarity:
Dest Local Similarity:
Query Match:
                                                                                1013
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1253 CATTICTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCAGGTTAAG 1312

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1223 AACGACCAGGTCATCGTGAAAATC 1246
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47.00
100.00%
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8.39%
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                  RESULT 5
US-09-873-637-18
US-09-873-637-18
Sequence 18, Application US/09873637
Sequence 18, Application US/09873637
Sequence 18, Application US/09873637
Setent No. US200200613434
Setent No. US200200613434
SEPENTRAL NTRORMATION:
TITLE OF INVENTION:
TITLE OF INVENTIO
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GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/873,637
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SSEQ ID NO 20
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Patent No. US20020061543A1
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49.00
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48.00
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ORGANISM: Mus musculus
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
Score:
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US-09-873-637-20
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1103 ATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAAC 1162
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Sequence 19, Application US/09873637
Patent No. US20202061543A1
GENERAL INFORMATION:
APPLICANT: ROSS, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960296-95131
CURRENT APPLICATION NUMBER: US/09/873,637
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
SEQ ID NO 19
TYPE: PRT
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                                                                                                                                                                    21 GluLeuGlnAsnLeuThrAlaAlaAlaGluValValValValProArgAspGlnThrProAspGlu 40
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                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09873637

Patent No. US20020061543A1

GENERAL INFORMATION:
TITLE OF INVENTION: HER C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE REPRENCE: 966296, 95131
CURRENT APPLICATION NUBER: US/09/873,637

CURRENT FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 17

LENGTH: 47
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Mismatches:
Indels:
US-09-270-437D-5 (1-1708) x US-09-873-637-20 (1-48)
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Matches:
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LENGTH: 422
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US-10-117-982-472

US-10-117-982-472

Sequence 472, Application US/10117982

Publication No. US20030138438A1

GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.

APPLICANT: Foy, Teresa M.

APPLICANT: Carter, Darrick

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Ralos, Michael D.

APPLICANT: Ralos, Michael D.

APPLICANT: Spies, Gregory A.

APPLICANT: Fan, Liqun

APPLICANT: Fan, Liqun

APPLICANT: Fan, Liqun

APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121-4555019

CURRENT FILING DATE: 2002-04-05

NUMBER OF SEQ ID NOS: 484

SEQ ID NO 472

TYPE: DOT

TYPE: DOT

TYPE: DOT

TYPE: DOT

TYPE: DOT

TYPE: DOT

THENTH: TOT

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; ORGANISM: Mus musculus US-09-873-637-19
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US-10-117-982-472
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Best Local Similarity:
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RESULT 10

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US-10-408-765A-2088
Sequence 2088, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Pahy, Eoin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTED
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC
TITLE OF INVENTION: DEBNIFIED IN THE MITOCHONDRIAL PROTEOME
TILE REPERENCE: 2003-04-04
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT APPLICATION NUMBER: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
Sequence 472, Application US/10313986
| Publication No. US20030236209A1
| GENERAL INFORMATION:
| APPLICANT: Poy, Teresa M.
| APPLICANT: MCNabb, Andria
| APPLICANT: Watanabe, Andria
| APPLICANT: Watanabe, Andria
| APPLICANT: Watanabe, Combosition of APPLICANT: Watanabe, Andria
| APPLICANT: Watanabe, ANDRIA CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER |
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ORGANISM: Homo sapiens
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ORGANISM: Homo
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McNeill, Patricia D.
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CRGANISM: Homo sapiens
US-09-850-716A-176
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                                     254 GTGGGTGCCATTATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGAGCGAG 313
                                                         APPLICANT: Railos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Panger, Gary R.
APPLICANT: Fanger, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Mang, Aijun
APPLICANT: Fanger, Neil
APPLICANT: Fanger, Neil
APPLICANT: Fanger, Neil
APPLICANT: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT FAPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SEQ ID NO 176
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                                                                                                              314 TCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAA 361
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US-09-270-437D-5 (1-1708) x US-10-408-765A-2088 (1-422)
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US-09-735-705-348
US-09-735-705-348
Sequence 348, Application US/09735705
Sequence 148, Application US/09735705
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fancer, Cary R.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Li, Samuel X.
                                                                                                                                                                                                                      Sequence 176, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
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Skeiky, Yasir A.W.
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Fan, Liqun
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US-09-735-705-176
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Best Local Similarity:
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US-09-735-705-176
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FR
LENGTH: 579
TYPE: RRT
CRGANISM: Homo sapiens
US-09-735-705-348
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US-09-850-7164-176
| US-09-850-7164-176
| Sequence 176, Application US/09850716A
| Patent No. US20020115139A1
| GENERAL INFORMATION:
| APPLICANT: Malos, Michael D.
| APPLICANT: Retter, Marc W.
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER; TILE REPRENCE: 210121.455015
| CURRENT FILING DATE: 2001-05-07
| NUMBER OF SEQ ID NOS: 440
| SEQ ID NO 176
| SEQ ID NO 176
| LENGTH: 579
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US-09-850-716A-348

| Sequence 348, Application US/09850716A |
| APPLICANT: Rates, Maccal D. |
| APPLICANT: Retter, Marc M. |
| TITLE OF INVENTION: CANCESTIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: CANCESTIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: CANCESTIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: CANCESTIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: CANCESTIONS AND METHODS FOR THE THERAPY |
| TOTRESTY FILING DATE: 2001 OG 07
| NUMBER: OF 06-07
| NUMBER: OF 06-07
| TYPE: PRT |
| TYPE: PRT
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Q9tu0 brachydanio
Q9uun bomo sapien
Q9uin homo sapien
Q9iiu homo sapien
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Q97zk6 streptococc
Q8cyy6 streptococc
Q9gmuy macaca fasc
Q93fz2 pectobacter
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Q80us9 mus musculu
Q42254 galllus gall
O73932 xenopus lae
O57526 xenopus lae
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O9cpn8 mus musculu
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O9y6m1 homo sapien
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Eom T., Singer R.H., Bassell G.J.;

Evaluating the strain of the strain s
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
B-actin zipcode binding protein 1.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TAXID=10116;
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QBB477
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\begin{array}{c} \text{LR} \\ \text{LR} \\
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Q8CGX0
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-MODEL=Frame+ n2p model - DEW=xlp
-COMM2L=Frame+ n2p model - DEW=xlp
-CGD2 1/USFTO_Spool p/US09270437/runat_13072004_121956_9981/app_query.fasta_1.1863
-DG=CGD2 1/USFTO_Spool p/US09270437/runat_13072004_121956_9981/app_query.fasta_1.1863
-DG=SPTREMBL_25 - OFWT=Fastan - SUFFIX=rspt - MINMATCH=0.1 - LOOPCL=0 - LOOPEXT=0
-UNITS=bits - START=1 - END=-1 - MATRIX=01igo - TRANS=human40.cdi - LIST=45
-NOTELGN=200 - THR SCORE=quality - THR MIN=1 - ALIGN=15 - MODE=LOCAL - OUTFMT=pto
-NORM=ext - FEARSIZE=500 - MINIEN=0 - MAXLENS=2000000000
-USER=US09270437 @CGN 1 1 146 @runat 13072004 111956_9981 - NCPU=6 - ICPU=3
-NOTELED - NGG SCORES=0 - WAIT - DSPBELOCK=100 - LONGLOG
-DGT TIMBOUT=120 - WARN TIMBOUT=30 - THRRADS=1 - XGAPOP=60 - XGAPEXT=60 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=60 - YGAPEXT=60 - DELOP=6 - DELEXT=7
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                       - protein search, using frame_plus_n2p model
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                 Euteleostomi;
Homo.
                                                                                     Ioannidis P., Trangas T., Dimitriadis E., Samiotaki M., Panoutsakopoulos G., Kyriazoglou I., Voutzoulias S., Tsiapalis Kittas C., Agnantis N., Pandis N.; Escopic expression of a KH domain containing protein, highly homologous to both human IMP-1 and mouse CRD-BP, in benign and
                                                                                                                                                         Interproject Court indiant incore can be in being in malignant mesenchymal tumors.;

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

-1-SIMILARITY: CONTAINS 4 FM DOMAINS.

EMBL, AF198254 AAF3703.1; -.

HISSP: P11940; LCVJ.

GO, GO:0003676; F:nucleic acid binding; IEA.

Interpro; IPR004087; KH dom.

Interpro; IPR004088; KH type.1.

Interpro; IPR004088; KH type.1.

Ffam; PF00013; KH; 4.

Ffam; PF00015; KH; 4.

SWART; SM00360; KH; 2.

SWART; SM00360; KH; 2.

SWART; SM00360; KR Type.1; 4.

PROSITE; PS50084; KR Type.1; 4.

PROSITE; PS50084; KR Type.1; 4.

PROSITE; PS50082; RRM; 2.

PROSITE; PS50082; RRM; 2.

PROSITE; PS50082; RRM; 2.

PROSITE; PS50082; RRM; 2.
                 Vertebrata; E; Hominidae;
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212
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                 Craniata, Ve
Catarrhini,
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   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
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Best Local Similarity:
Query Match:
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SEQUENCE FROM N.A.
                                            NCBI_TaxID=9606;
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Pred. No.:
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Pfam; PF00076; rrm; 2.
SMART; SM0322; KH; 4.
SMART; SM0360; RRM; 2.
PROSITE; PS5004; KH TYPE 1; 4.
PROSITE; PS50102; RRM; 2.
SEQUENCE 577 AA; 63436 MW; 0647676128FBDIEE CRC64;
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QNZI8;
QNZI8;
QNZI8;
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
mRNA-binding protein CRDBP.
                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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SEQUENCE FROM N.A.
MEDINE-94179348; PubMed-8132663;
Prokipcak R.D., Herrick D.J., Ross J.;
Prokipcak R.D., Herrick D.J., Ross J.;
"Purification and properties of a protein that binds to the C-terminal coding region of human c-myc mRNA..;
J. Biol. Chem. 269:9261-9269(1994).
                                                                                                                                                                     314 SerbeuglnAspLeuThrbeuTyrAsnProgluArgThrIleThrValLysGlyAlaile
274 AlaAspGluValProLeuLysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGly
                                                                                                                                             575 TCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGCCCATC
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MEDLINE=21085660; PubMed=112.7851;
MEDLINE=21085660; PubMed=112.7851;
MEDLINE=21085660; PubMed=112.7851;
Aravai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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Wakaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
VCBI_TaxID=10090;
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MEDLINES 9732234; PubMed=9178888;
MEDLINES 9732234; PubMed=9178888;
Ledds P., Kren B.T., Boylan J.M., Betz N.A., Steer C.J.,
Gruppuso P.A., Ross J.;
"Developmental regulation of CRD-BP, an RNA-binding protein that
stabilizes C-myc mRNA in vitro.";
Oncogene 14:1279-1286(1997).
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MEDLINE=92217743; PubMed=1559612;
Bernstein P.L., Herrick D.J., Prokipcak R.D., Ross J.;
Bernstein G. — Harrick D.J., Prokipcak R.D., Ross J.;
"Control of G.— myc mRNA half-life in vitro by a protein capable binding to a coding region stability determinant.";
Genes Dev. 6:642-654(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDING = 8114742;
MEDILINE = 94158886; PubMed = 8114742;
Herrick D.J., Ross J.;
"The half-life of c-myc mRNA in growing and serum-stimulated influence of the coding and 3' untranslated regions and role
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Fleisig A.J.; Bubmitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Coding region determinant binding protein.
IGF2BP1 OR CRDBP.
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Ross J., Prokipcak R.D., Leeds P., Doyle G.A.R.,
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Mol. Cell. Biol. 14:2119-2128(1994).
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                                                           546 SerGinMetAlaGinArgLysIleArgAspileLeuAlaGinValLysGinGinHisGin 565
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SEQUENCE FROM N.A.

STRAILESTBL/6J;

MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

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                              AGTCAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAG
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Insulin-like growth factor 2.
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334 GluasnCysCysArgAlaGluGlnGluIleMetLysLysValargGluAlaTyrGluAsn 353
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Strausberg R.;
Strausberg R.;
Strausberg R.;
Submittee (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC051679; AAH51079.1;
GO; GO:003676; F:nucleic acid binding; IEA.
R. InterPro; IPR004089; KH dom.
R. InterPro; IPR004089; KH ± type 1.
R. InterPro; IPR004089; KH ± to micerPro; IPR004089; KH; 4.
R. Fam; PF00013; KH; 4.
SMART; SM00320; KH; 4.
SMART; SM00320; KH; 2.
RRMART; SM00320; RRM; 2.
RRGUENCE 577 AA; 63378 MM; D439F544257DA3CE CRC64;
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SEQUENCE FROM N.A.
STRAIN=129/Sv x 129/Sv-CP; TISSUE=Embryonic stem cells;
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STRAIN=129/Sv x 129/Sv-CP; TISSUE=Embryonic stem cells;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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983 CGTATGGTTATCATCACTGGACCGCCGAGGCCCCAATTCAAGGCTCAGGGAAGAATCTAT 1042
                          GCATCAGCAGCTGGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAAACGAGTTGCAGAAT 1174
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                                                495 AlaSerAlaAlaGlyArgValIleGlyLySGlyGlyLySThrValAsnGluLeuGlnAsn 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 ArgMetValileIleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArglleTyr 484
475 GluGluAsnPhePheGlyProLysGluGluValLysLeuGluThrHisIleArgValPro 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyLysLeuLysGluGluAsnPhePheGlyProLysGluGluValLysLeuGluThrHis
                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VG1 RNA binding protein variant D.
VG1 RNA binding protein variant D.
Eukaryots, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae, Xenopus.
                                                                           1175 TTGACGCCAGCTGATGGTACCAAGAGACCAGACCCCTGATGAGAAC 1225
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A MEDLINE=9922831; PubMed=9560341;
A MEDLINE=9922831; PubMed=9560341;
A Mighly conserved RNA-binding protein for cytoplasmic mRNA collization in vertebrates.";
I Callization in vertebrates.";
I Ocalization in vertebrates.";
I Ocalization in vertebrates.";
I Ocalization in vertebrates.";
I MEDI, 8409-496(1998).
I Ocalization in vertebrates.";
REMBL, AF05823; AAC12859.1;
REMBL, AF05823; AAC12859.1;
ROGO, GO:0003674; F:nucleic acid binding; IEA.
RILEPRO, IPR004088; KH_type_1.
R InterPro; IPR000504; KN_Type_1.
R Pfam; PF00076; rrm; 2.
R SWART; SM00362; KN, 4.
R SWART; SM00362; KN, 2.
R SWART; SM00362; KN, 2.
R SWART; SM00360; RRM; 2.
                                                                                        515 LeuThrAlaAlaGluValValValVaProArgAspGlnThrProAspGluAsn 531
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0 0 0 0 0
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PROSITE; PS50102; RRM; 2.
SEQUENCE 594 AA; 65643 MW· F
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                                                                           1174
                                                                                                                              TTGACGGCAGCTGAGGTGGTAGTACCAAGAGCCGGACCCCTGATGAGAACGACCAGGTC 1234
                                                                                                                                                                                ATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCGAGAC 1294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 IleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArglleTyrGlyLysLeuLys 474
456 IleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArglleTyrGlyLysLeuLys 475
                                      GluGluAsnPhePheGlyProLysGluGluValLysLeuGluThrHislleArgValPro
                                                                           GCATCAGCAGCTGGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAAT
                                                                                                                                             Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                 ATCCTGGCCCAGGTTAAGCAGCACCATCAGAAGGGACAGAGTAAC 1339
                                                                                                                                                                                                                                                  556 IleLeuAlaGlnValLysGlnGlnHisGlnLysGlyGlnSerAsn 570
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Last annotation update)
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Best Local Similarity:
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NCBI_TaxID=9031;
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Pred. No.:
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254 GTGGGTGCCATTATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCCAG 313
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MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

The FANTOM COnsortium,

The FANTOM Consortium,

The FANTOM Consortium;

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

Nature 420:563-573 (2002).

MALUS $420:563-573 (2002).

MGD; MGI:1890359; Igf2bp3.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 SerLysileAspValHisArgLysGluAsnAlaGlyAlaAlaGluLys 242
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                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPRO04089; XH dom.
InterPro; IPRO04088; XH dom.
InterPro; IPRO04088; XH dom.
InterPro; IPRO04088; XH type_1.
InterPro; IPRO0504; RNA_rec_mot.
Pfam; PPO0015; XTm; 2.
SMART; SM00320; RH; 4.
SMART; SM00360; RRM; 2.
PROSITE; PS50084; KH TYPE_1; 4.
PROSITE; PS50003; RRM; NNP 1; PALSE NEG.
PROSITE; PS00030; RRM; NNP 1; PALSE NEG.
SRQUENCE 579 AA; 63720 MW; AESG3A8EE3C135C5 CRC64;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Insulin-like growth factor 2.
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Matches:
Conservative:
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Indels:
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                                                                              Mueller-Pillasch F., Lacher U., Wallrapp C.,
Oncogene 0:0-0(0).
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                                                              SEQUENCE FROM N.A.
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Best Local Similarity:
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                      NCBI_TaxID=9606;
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01-0TN-1998 (TERMELTE). 25, Last annotation update)
KH domain-containing transcription factor B3.
Kenopus lavis (African clawed frog).
Eukaryota: Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=92249652; PubMed=1577195;
Pfaff S.L., Taylor W.L.;
"Characterization of a Xenopus oocyte factor that binds to a Gratzedlephratiation of a Xenopus ocyte factor that binds to a Developmentally regulated cis-element in the TFIIIA gene.";
Dev. Biol. 151:306-316(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Griffin D., Taylor W.L.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Havin L., Git A., Elisha Z., Oberman F., Yaniv K.,
Havin L., Git A., Elisha Z., Oberman F., Yaniv K.,
Havin L., Git A., Elisha Z., Oberman F., Yaniv K.,
Genes Dev. O:0-0(1998).

-1- SIMILARITY: CONTAINS 4 KH DOMAINS.
EMEL, AF0642353; AAB99457.1; -.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR004089; KH dom.
InterPro; IPR004089; KH dom.
InterPro; IPR00504; KH, 4.
InterPro; IPR00504; KH, 4.
Efam; PP00013; KH, 4.
SYART; SW00322; KH, 4.
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PROSITE; PS50102; RRM, 2.
PROSITE; PS00030; RRM RNP_1; PALSE_NEG.
SEQUENCE 593 AA; 65385 MW; 5A5AB4B4A1D55DF7 CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 05, Last annotation update)
Putative RNA binding protein KOC (KOC).
KOC.
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Matches:
Conservative:
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                      PRT;
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Query Match:
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O57526
ID O57526 P
AC O57526;
DT 01-JUN-1998 (
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AC Q9PW80
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SEQUENCE FROM N.A.

REALW-C57BL/6J; TISSUE=Embryo;

REALW-C57BL/6J; TISSUE=Embryo;

REALWAR J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawal J., Shinagawa A., Shibata K., Yoshino M., Ttoh M., Ishii Y.,

A Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Radota K., Matsaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsudi H., Saitoki R., Tomita M., Wagner L., Washio J.,

Rubell P., Lewis S., Matsuo Y., Nikaido I., Ring B., Kochiwa H.,

Rubell P., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Bakai K., Okido T., Furuno M., Anno H., Baldaralli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Basaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Rusuki H., Toyo-Oka K., Wang K.H., Weitz C., Wilttaker C., Wilming L.,

Basaki Y., Toyo-Wa K., Wang K.H., Weitz C., Wilttaker C., Wilming L.,

Hyashizaki Y., Toyo-Wa K., Wang K.H., Weitz C., Wilttaker C., Wilming L.,

Hyashizaki Y., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                          207 ValGlyAlaIleIleGlyLysGluGlyAlaThrIleArgAsnIleThrLysGlnThrGln 226
                                                                                                                                                                                                                                                                                                                         GTGGGTGCCATTATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCCAG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 12, Last sequence update)
10 days embryo CDNA, RIKEN full-length enriched library,
clone: 2610036B18, full insert sequence (Igf2 mRNA-binding protein 3)
[Insulin-like growth factor 2, binding protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mori H., Sakakibara S., Imai T., Nakamura Y., Iijima T., Suzuki A.,
Yuasa Y., Takeda M., Okano H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotation of a full-length mouse cDNA collection.";
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR004089; KH dpm.
InterPro; IPR004089; KH Type_1.
InterPro; IPR004084; RNA_rec_mot.
Pfam; PF00013; KH; 4.
Pfam; PF00076; rrm; 2.
SNART; SM00325; KH; 4.
SNART; SM00350; RRM; 2.
PROSITE; PS50084; RM; 2.
PROSITE; PS50102; RRM; 2.
PROSITE; PS50102; RRM; 2.
SRQUENCE 579 AA; 63551 MW; 937E601A95D06B77 CRC64;
                                                                                                                                                                                         579
30
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0
                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                  TCCAAGATAGACGTGCATAGGAAGGAGAAC 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        579 AA
                                                                                                                                                                                                                                                  Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                        1.24e-21
30.00
100.00%
                                                                                                                                                                                                                                                  5.36%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                  314
                                                                                                                                                                                                                                                                                                                                                                                                             227
                                                                                                                                                                                                                                                 Query Match:
DB:
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                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN=CSTBL/6; TISSUE=Brain, and Olfactory epithelium;
WEDLINE=22388257; PubMed=12477932;
WASTAIN=CSTBL/6; TISSUE=Brain, and Olfactory epithelium;
WASTAIN=CSTBL/6; TISSUE=Brain, and Olfactory epithelium;
WASTAIN=CSTBL, Felingeld E.A., Grouse L.H., Derge J.G.,
Altschul S.P., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,
Altschul S.P., Moran H., Moore T., Max S.I., Wang J., Haiteh F.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., McKerran K.J., Mallek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rokrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGGTGCCATTATTGGCAAGGAGGGGCCACCATCCGCAACACACAAACAGCCCAG 313
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"Expression of mouse igf2 mRNA-binding protein 3 and its implications for the developing central nervous system."; J. Neurosci. Res. 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGG; GO: 00036/6; F: mucleic acid binding; IEA.

InterPro; IPR004088; KH dom.

InterPro; IPR004088; KH type_l.

InterPro; IPR004088; KH type_l.

Pfam; PF00013; KH; 4.

R SMART; SM00302; KH; 4.

R SMART; SM00304; KH TYPE_l; 4.

R PROSITE; PS50084; KH TYPE_l; 4.

R PROSITE; PS50084; KH TYPE_l; 4.

SEQUENCE 579 AA; 63574 MW; CABD9A4355B392B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strandsorg R.;
Strandsorg R.;
Submitted (WAR-2003) to the EMBL/GenBank/DDBJ databases.
- SIMILARITY: CONTAINS 4 KH DOMAINS.
- SIMILARIY: CONTAINS 4 KH DOMAINS.
- SIMILARIY: ARO1669; BARD17779.1; -.
EMBL; ARO16613; BARD19755.1; -.
EMBL; BC045139; AAH45082.1; -.
MGJ; MGJ:1890359; Igf2bp3.
GO; GO:0003676; Finucieic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain, and Olfactory epithelium;
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30
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLysileAspValHisArgLysGluAsn 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    582
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30.00
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01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity:
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DI-GWY-2003 (TERBAILE, 13, Last expense update,)

DI-GWY-2003 (TERBAILE, 13, Last annotation update,)

DE 901-007-2003 (TERBAILE, 13, Last annotation update,)

DE 902-2003 (TERBAILE, 13, Last annotation update,)

DE 102-2003 (TERBAILE, 13, Last annotation,)

DE 102-2003 (TERBAILE, 13, Last annotation,
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277 ProLeulysIleLeuAlaHisAsnAsnPheValGlyArgLeulleGlyLysGluGlyArg 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          983 CGTATGGTTATCATCACGCCGCCAGAGGCCCAATTCAAGGCTCAGGAAGAATC 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 ArgMetValllelleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArglle 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Xu C.S., Li W.Q., Li Y.C., Yang K.J., Yan H.M., Chang C.F., Zhao L.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                        Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                 61842 MW; 1EDEFB100443DDC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hepatocellular carcinoma autoantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.87e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.00
100.00%
100.00%
3.39%
                              527 AACCTGAAGAAG 538
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                  556 AA;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                           Q9Y6M1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
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Q7TP50
                                                                      RESULT 13
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Length:
Matches:
Conservative:
Mismatches:

2.3e-15 24.00 100.00% 100.00% 4.29%

> Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

Indels: Gaps:

US-09-270-437D-5 (1-1708) x Q9PW80 (1-582)

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RECUENCE FROM N.A.

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE-Brain;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Aptensko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RA Villalon D.K., Muzry D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Hellon E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

A Jones S.J., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.",

Phoc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Ma H., Wang L., Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
"Liver regeneration after PH.";
Subintred (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY328199; AAP928601.1; --
SEQUENCE 169 AA; 17743 MW; 19BF6295C1000CBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Muscullarandellosso;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054552; AAH54552.1; -.
Hypochetical protein:
SEQUENCE 545 AA; 59679 MW; 88DD35FF30DF3091 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 545
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.85e-06
15.00
100.00%
100.00%
2.68%
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16.00
100.00%
100.00%
2.86%
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                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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Search completed: July 13, 2004, 12:34:38 Job time : 100 secs

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Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 170, Appli Sequence 170, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 34, Appli Sequence 34, Appli Sequence 296, Appli Sequence 31, Appli Sequence 31, Appli

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APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Glockert, Elisabeth
APPLICANT: Found, Alexander
APPLICANT: Glockert, Elisabeth
APPLICANT: Glockert, Elisabeth
APPLICANT: Hasharder
APPLICANT: Hasha
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US-08-68-137-1
US-08-470-145-1
US-08-477-389-1
US-08-340-428B-1
PCT-US9-107306-1
US-08-956-171E-170
5188088-1
US-09-479-128-1
US-09-479-128-1
US-09-103-840A-1
US-09-26-103-840A-1
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Pred. No. 0;
; Mismatches
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Sequence 5, Application US/09061709B

Patent No. 6297364

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                  1 agggacgctgccgcaccgcc......atttccttcaggttttaaaa 1708
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-25-991A-7254

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DB 3; Length 1708; 0; Indels

00	ncleic Acid Molecules Encodi 1 1:he Antigens Per Se, And Use 09/899,651 6/061,709	Query Match
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1.2%; Score 20; DB 4; Length 1740;
100.0%; Pred. No. 4;
tive 0; Mismatches 0; Indels
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APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
WUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                      GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Falo, inchael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Panger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: US/09/542,615A
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
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                US-09-542-615A-347
; Sequence 347, Application US/09542615A
; Patent No. 6518256
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US-09-606-421B-347
; Sequence 347, Application US/09606421B
; Patent No. 6531315
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APPLICANT: Wang, Tongrong
APPLICANT: Fan, injun:
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosker, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: In', Samuel X.
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Best Local Similarity 100.0
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-09-542-615A-347
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LENGTH: 1740
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SEQ ID NO 347
LENGTH: 1740
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APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McMeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 20; DB 4; Length 1740;
100.0%; Pred. No. 4;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.1;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Oligonucleotide primer US-09-261-855-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1178 ACGCCAGCTGAGGTGGTAGTACC 1200
508 CATTGGCAAGGAAGGACGGAACCT 531
                                     24 CATTGGCAAGGAAGGACGGAACCT 1
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Patent No. 6426072
GENERAL INFORMATION:
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Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aljun
Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA .
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 20; Conserva
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranos, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Moneill, Particia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT PILLING DATE: 2000-08-21
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEALURE:
FEALURE:
FORTION: (3347)
OTHER INFORMATION: n=A,T,C or G
NAME,KEY: unsure
LOCATION: (3502)
OTHER INFORMATION: n=A,T,C or G
NAME,KEY: unsure
LOCATION: (3506)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3500)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3520)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3538)
OTHER INFORMATION: n=A,T,C or G
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LOCATION: (3940)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3968)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3978)
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OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4056)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4062)
OTHER INFORMATION: n=A,T,C or G
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OTHER INFORMATION: n=A,T,C or
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OTHER INFORMATION: n=A,T,C or
                     Tongtong
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Wang, it.
Ligun
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) LOCATION: (4088)
) OTHER INFORMATION: D:
) NAME/KEY: unsure
) LOCATION: (4115)
) OTHER INFORMATION: D:
US-09-643-597-175
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NAME/KEY: unsure
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LOCATION: (4080)
OTHER INFORMATION:
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LOCATION: (3646)
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                             FARENAL INFORMATION:
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Tsang, Solam
APPLICANT: Tsang, Solam
APPLICANT: Tsang, Solam
APPLICANT: Muth, Alexander
APPLICANT: Old, LiOyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
TITLE OF INVENTION: Assign, The Antigens Per Se, And Uses Thereof
FILE REPERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
IENGTH: 4159
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Parent No. 657656

GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Else
APPLICANT: Stockert, Else
APPLICANT: Mager, Elke
APPLICANT: Old, iloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer;
TITLE OF INVENTION: Associated
CURRENT APPLICATION NUMBER: US/09/061,709
PRIOR PLING DATE: 2001-07-06
PRIOR PLING DATE: 1998-04-17
NUMBER: OF SEQ ID NOS: 8
SEQ ID NOS: 8
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1.2%; Score 20; DB 4; Length 4159;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels
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US-09-643-597-175
IS-09-e46-57-5 Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-09-899-651-4
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US-09-899-651-4
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Query Match 1.2%; Score 20; DB 4; Length 4181; Best Local Similarity 100.0%; Pred. No. 4.2; Matches 20; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                           RESULT 14
US-09-480-884A-175
Sequence 175, Application US/09480884A
Sequence No. 6482597
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Hosken, Nancy A.
APPLICANT: Aclos, Michael D.
APPLICANT: Aclos, Michael D.
APPLICANT: Aclos, Michael D.
APPLICANT: Aclos, Michael D.
APPLICANT: Alogev, Compounds and Applicant: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121-452CG
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 175
LENGTH 4181
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US-09-542-615A-175
Sequence 175, Application US/09542615A
Patent No. 651826
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitenya S.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.4556
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE FERSESCE FERSESCE FOR WINDOWS Version 3.0
                                                                                        1019 ITCAAGGCTCAGGGAAGAAT 1038
                                                                                                                    1640 TTCAAGGCTCAGGGAAGAAT 1659
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; LOCATION: (1)...(4181)
; OTHER INFORMATION: n=A,T,C or G
US-09-480-884A-175
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LOCATION: (3347)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3502)
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ORGANISM: Homo sapiens
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LENGTH: 4181
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LOCATION: (4062)
COTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4080)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4080)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
                 NAME/KEY: unsure
COCATION: (3506)
COTHER INPORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3520)
COTHER INPORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3538)
OTHER INPORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3549)
OTHER INPORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3646)
OTHER INPORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3340)
OTHER INPORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3340)
OTHER INPORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3368)
OTHER INPORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3368)
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LOCATION: (4036)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4056)
OTHER INFORMATION: n=A,T,C or G
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), OTHER INFORMATION: n=A,T,C or G
US-09-542-615A-175
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LOCATION: (3974)
OTHER INFORMATION: n=A,T,C or
n=A, T, C
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Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Tylopoda; Camelidae; Camelus
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15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
                                                                                                                                                                                   ALIGNMENTS
                                                 CBGR CLOAB
LLV27_HUWAN
GWUI HALMI
RLA2_BRUWA
A31_VACCV
VA31_VACCV
VA31_VACV
VA31_VACV
VA31_VACV
C17_HUWAN
FLIS_VIBCH
VA31_VARV
VA31_VARV
VA31_VARV
HS11_SCOYEN
HS11_SCOYEN
                  RYR1_HUMAN
RL32_VIBCH
RM33_YEAST
FIS_ERWCA
FIS_YERPE
CBGR_CLOAB
                                                                                                                          CHICK
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STANDARD;
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Mammalia; Eutheria;
NCBI_TaxID=9837;
 CAMBA
                                                                                                                                                                                               RESULT 1
ING CAMBA
0 0 0 0 0 0 0 0 0
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                                               (without alignments)
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                                                                              agggacgctgccgcaccgcc......atttccttcaggttttaaaa 1708
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Compugen Ltd.

    protein search, using frame_plus_n2p model

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      GenCore version (c) 1993 - 2004
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Ygapext 60.0
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OCRB_BACTC
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                                         July 13, 2004, 12:14:48
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                                                                  US-09-270-437D-5
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yersinia pe clostridium homo sapien halobacteri

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Readan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,
A Gunda M.;
Cloning and sequence analysis of cytokine cDNAs of llama and camel.";
T "Cloning and sequence analysis of cytokine cDNAs of llama and camel.";
T "Cloning and sequence analysis of cytokine cDNAs of llama and camel.";
T. Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
C or mitogens. IFN-gamma, in addition to having antivital activity,
has important immunoregulatory functions. It is a potent activator
C of macrophages, it has antiproliferative effects on transformed
C cells and it can potentiate the antiviral and antitumor effects of
C cells and it can potentiate the antiviral and antitumor effects of
C cells and it can potentiate the antiviral and antitumor effects of
C cells ENGINIT: Homodimer (By similarity).
C :- SUBGNIT: Homodimer (By similarity).
C :- SUBGNIT: Released primarily from activated T This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch) lymphocytes. SIMILARITY: Belongs to the type II (or gamma) interferon family. EMBL; AB107657; BAC75394.1; -. InterPro; IPR002069; IFN-gamma. Pfam; PF00714; IFN-gamma; 1. ÷

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Length:
Matches:
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Mismatches:
Indels:

Gaps:

AspValAlaAspGlyGlyProLeu 51 STANDARD; ING LAMGL RESULT 2 ò

Lama glama (Llama). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Lama. 15-MAR-2004 (Rel. 43, Created) 15-WAR-2004 (Rel. 43, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update) Interferon gamma precursor (IFN-gamma). PRT; 166 AA SEQUENCE FROM N.A. NCBI\_TaxID=9844; 

"Cloning and sequence analysis of cytokine cDNAs of llama and camel.", Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Produced by lymphocytes activated by specific antigens or mitogens. IFN-gamma, in addition to having antiviral activity, has important immunoregulatory functions. It is a potent activator of macrophages, it has antiproliferative effects on transformed cells and it can potentiate the antiviral and antitumor effects of the type I interferons (By similarity).
-! SUBUNIT: Homodimer (By similarity). Raadan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C., Onuma M.;

-!- SUBCELLULAR LOCATION: Secreted (By similarity).

lymphocytes. -!- SIMILARITY: Belongs to the type II (or gamma) interferon family.

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INTERFERON GAMMA.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

239378814759328F CRC64; Cytokine, Antiviral, Growth regulation, Glycoprotein, Signal. SIGNAL 1 20 BY SIMILARITY. InterPro; IPR002069; IFN-gamma. Pfam; PF00714; IFN-gamma; 1. ProDom; PD002435; IFN-gamma; 1. 21 166 IN 39 39 N-: 106 106 N-: 166 AA; 19475 MW; CARBOHYD CARBOHYD SEQUENCE

Alignment Scores:

us-09-270-437d-5.rsp

1,66 0000 0000 Conservative: Mismatches: Length: Matches: Indels: Gaps: 36.5 8.00 100.00% 100.00% 1.448 Percent Similarity: Best Local Similarity: Query Match: Pred. No.:

US-09-270-437D-5 (1-1708) x ING\_LAMGL (1-166)

Bacteria, Firmicutes, Bacillales, Bacillaceae, Geobacillus. Menaquinol-cytochrome c reductase cytochrome B subunit 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 224 AA PRT; STANDARD; SEQUENCE FROM N.A. STRAIN=K1041 BACTC 045658; KESULT 3 QCRB\_BACTC QCRB 

protein (By similarity).
--- Subdunt: THE MAIN SUBGNITS OF THE MENAQUINONE:CYTOCHROME C COMPLEX ARE: CYTOCHROME B, THE RIESKE PROTEIN AND A 22/29 KDa CYTOCHROME B/C SUBGNIT. MEDLINE=96218169; PubMed=8647852; Sone N., Tauchiya N., Inoue M., Noguchi S.; "Bacillus stearothermophilus qur operon encoding Rieske FeS protein, cytochrome b6, and a novel-type cytochrome c1 of quinol-cytochrome c reductase.", "J. Biol. Chem. 271:12457-12462(1996). complex.

-i- SUBCELLUTAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY. CORRESPONDS TO THE AMINO END OF MITOCHONDRIAL CYTOCHROME B.

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Alignment Scores:

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Fabret C., Quentin Y., Chapal N., Guiseppi A., Haiech J., Denizot F.,
"Integrated mapping and sequencing of a 115 kb DNA fragment from
Bacillus subtilis: sequence analysis of a 21 kb segment containing
the sigl locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Denizot F., Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                         YVEL BACSU STANDARD; PRT; 227 AA. P7151, 008170, 008170, 108170, 108170, 28-FEB-2003 (Rel. 41, Last sequence update) 10.0077-2003 (Rel. 42, Last annotation update) 10.0079 (Rel. 42, Last annotation vpdate) 10.0079 (Rel. 42, Last annotation vpdate) 10.007933360.
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ID YCBC ECOLI

STANDARD; PRT; 259 AA.

AC P36555; P75846;

DT 01-UTN-1994 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DT 16-COT-2001 (Rel. 40, Last annotation update)

DT WCBC OR B0920 OR Z1267 OR ECS1003.

GN YCBC OR D0920 OR Z1267 OR ECS1003.

GS Escherichia coli, and

OS Escherichia coli O157:H7.

OC Enterobacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC NCBL TaxID=562, 83334;
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Sampoi G., Saki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                         CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A70036; A70036.
Subtilist: BG11860; YveL.
InterPro; IRG01007; EPS synthesis.
TIGRPAMs; TIGR01007; eps_fam; 1.
TIGRPAMs; TIGR01007; Transferase; Tyrosine-protein kinase;
Complete proteon; Transferase; Tyrosine-protein kinase;
SEQUENCE 227 AA; 24674 MW; 81C8B9D75278FPA9 CRC64;
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"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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                                                                                        SIMILARITY: Belongs to the cpsD/capB family.
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EMBL; Z94043; CAB08024.1; -.
EMBL; Z99121; CAB15441.1; -.
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us-09-270-437d-5.rsp

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RESULT 6
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ENEL; AE00194; AAC74000.

ENEL; AE00530; BAA35666.1; -.

ENEL; D90730; BAA35666.1; -.

R EMEL; D20440; -; NOT_ANNOTATED_CDS.

DR PIR; O20754; C90754.

DR PIR; G64831; G64831.

DR ECGGene; EG12166; ycbC.

DR Enterpro; IRRO3848; D107218.

DR ENTERPRO3848; D107218.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=0157:17 / RIND 0509952;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12:";
                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=O157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074933; PubMed=11206551;

MEDLINE=21074933; PubMed=11206551;

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatifick H.A., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatifick H.A., Grosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Melch R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94232180; PubMed=7513784;
Feng J., Yamanaka K., Niki H., Ogura T., Hiraga S.;
"New Kiling system controlled by two genes located immediately
upstream of the mukB gene in Escherichia coli.";
Mol. Gen. Genet. 243:136-147(1994).
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Indels:

.448

Query Match:

US-09-270-437D-5 (1-1708) x YCBC\_ECOLI (1-259) 479 GGATCTTCAGGGGAACCTCGTCAG 456 251 GlySerSerGlyGluProArgGln 258

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RC STRAIN=Berkeley;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Richards S., Abburner M., Henderson S.N.,

Ra Gorge R.A., Lewis S.E., Richards S., Abburner M., Henderson S.N.,

RA Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,

Ration R.G., Rogers Y.H.C., Blazej R.G., Change M., Pielifer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pannkoch C. Baidwin D.,

RA Beson K.Y., Benos P.V., Barman B.P., Bhandari D., Bolshakov S.,

RA Beris K.C. Busam D.A., Burller H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Butler M.R., Bouck J., Brokstein P., Brother P., Candra I.,

RA Gebook K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Bris B., Delcher A., Dahlke C., Davenport L.B., Davics P.,

RA Gebook K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Goson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Harris N.L., Favrey D.A., Heniman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heniman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Mouse D.A., Howland T.J., Wei M.-H., Ibigame C.,

RA Harris N.L., Mouse M., Mordry C., Morris J., Moshref B.,

RA Liu X., Matteri B., Morthook T.C., McLeod M.P., McPherson D. L.,

RA Liu X., Matteri B., Moy M., Murphy B., Mirphy L., Muzry D.M., Noshrefi B.,

Reinert X., Remington K., Saunders R., Deltard J., Puri V., Reese M.G.,

Reinert X., Remington K., Saunders R., Uenter E., Wang K., Shen B.,

Rand S.M., Woodage T., Singeon M., Strong R., Sun B.,

Rand S.M., Woodage T., Singeon M., Zhang G., Zhao G., Zhen J.,

Rand S.M., Woodage T., Stupen G., Worler B., Wang K.,

Rand S.M., Woodage T., Stupen G., Worler B., Wang G., Zhen K.,

Rand S.M., Woodage T., Worley C., Worler B., Wang G., Zhen K.,

Rand S.M., Woodage T., Worley C., Worler B., Wang G., Shen B.,

Rand S.M., Woodage T., Worley C., Wood G., Zhen R.,

R
                                                                                                                                                                                                                                                                                                                                     Cramton S.E., Laski F.A.; "String of pearls encodes Drosophila ribosomal protein S2, has Minute-like characteristics, and is required during oogenesis."; Generics 137:1039-1048(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila.";
Nucleic Acids Res. 21:351-351(1993).
--- SIMILARITY: Belongs to the S5P family of ribosomal proteins.
--- SIMILARITY: Contains 1 S5 DRBM domain.
                                                                                                                                              Drosophila melanogater (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Phydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barrio R., del Arco A., Cabrera H.L., Arribas C., "Cloning and analysis of the S2 ribosomal protein cDNA from
RS2_DROME STANDARD; PRT; 267 AA. P31009; Q9VL74; STANDARD; Created) 01-UTL-1993 (Rel. 31, Last sequence update) 10-OCT-2003 (Rel. 31, Last sequence update) 40S ribosomal protein S2 (Strings of pearls protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Canton-S;
MEDLINE=93181212; PubMed=8441641;
                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A. MEDLINE=95073591; PubMed=7982558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-241 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=20294882; PubMed=10833454;
Matsumoto M., Saito T., Takasaki J., Kamohara M., Sugimoto T.,
Robayasahi M., Tadokoro M., Matsumoto S., Ohishi T., Furnichi K.;
"An evolutionarily conserved G-protein coupled receptor family, SREB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                  S5 DRBM.

GG -> PP (IN REF. 3).

K -> R (IN REF. 3).

ADA22CD28F100743 CRC64;
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Matches:
Conservative:
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation update)
SREBE.
                                                                                                                                                                                                                                                                                                                                                                                                    371 AA
                                                                                                                                                                                                                                                                                                     Indels:
                                                                      US-09-270-437D-5 (1-1708) x RS2_DROME (1-267)
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                                                                                                                                                                                                                                                                                                                                                          28899 MW;
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100.00%
100.00%
1.43%
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                                                                                                                                                                                                                                          267 AA;
                                                                                                                                                                                                         Ribosomal protein.
                                                                                                                                                                                                                                                                                              Best Local Similarity:
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                                                                                                                                                                                                                                                                                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                          GP85_BRARE
ID GP85_BRARE
AC Q91919;
                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                           SEQUENCE
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DB:
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                               Score:
8
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAPHTHOATE.
SUBCELLUIAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97474276; PubMed=9335300;
Mabuchi T., Hazayama S.;
Mabuchi T., Hazayama S.;
"Biochemical and genetic characterization of 2-carboxybenzaldehyde dehydrogenase, an enzyme involved in phenanthrene degradation by Moscardioldes sp. strain KP7.";
J. Bacteriol. 179:6488 6594 (1997).
-:- FUNCTION: PROBABLY INVOLVED IN THE TRANSPORT OF 1-HYDROXY-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .) (POTENTIAL)
.) (POTENTIAL)
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Nocardioides sp. (strain RP7).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Propionibacterineae, Nocardioideceae, Nocardioidece.
NCBI_TaxID=35761,
                                                                         EMBL; AB040805; BAA96651.1; -.
ZEIN; ZBB-GENBE-000710-2; sreb2.
InterPro; IBR000276; GPGR_Rhodpsn.
PRINTS; PR00021; 7tm_1; 1.
PRINTS; PR00237; GPGRAHODPSN.
PROSTTE; PS00237; GPROTEIN RECEP_F1_2; 1.
PROSTTE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.

26 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                     3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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P6F6175ED3A348C2 CRC64;
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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Matches:
Conservative:
Mismatches:
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15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 N
41954 MW;
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100.00%
100.00%
1.44%
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Best Local Similarity:
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288
309
322
343
95
95
183
371 ½
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024723;
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DISULFID
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SEQUENCE
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SEQUENCE FROM N.A.
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Y018 MYCGE
                                                                                                                                                                                                                                                                               Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;

    -!- SIMILARITY: Belongs to the sugar transporter family.

                                                                                                                                                                                          1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
2 (POTENTIAL).
                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                          7 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                   11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                  InterPro; IPR007114; MFS.
InterPro; IPR007114; MFS.
InterPro; IPR005829; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
PEam; PF00083; Sugar tr; IPR005083; Sugar tr; IPR051TE; PS00816; SUGAR TRANSPORT 1; IPR0501TE; PS00216; SUGAR TRANSPORT 2; FALSE NEG.
PROSITE; PS00217; SUGAR TRANSPORT 2; FALSE NEG.
PRANSPORT; Transmembrane; Inner membrane.
DOMAIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                               9 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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D6D765D376260D8A CRC64;
                                                                                                                                                                                                              2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nonsyndromic hearing impairment protein 5 homolog.
DFNAS OR DFNASH.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1217 CAGGGGTCTGGTCTTGGTACTA 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 GlnGlySerGlyLeuLeuValLeu 284
                                                                                            EMBL; AB000735; BAA23264.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                          49109 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
100.00%
1.44%
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Best Local Similarity:
Query Match:
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DFNS MOUSE
ID DFNS MOUSE
Q922D3;
COT-200;
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Pred. No.:
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                                                           Van Laer L., Huizing E.H., Verstreken M., van Zuijlen D., Wauters J.G., Bossuyt P.J., Van de Heyning P., McGultr W.T., Smith R.J.H., Willems P.J., Legan P.K., Richardson G.P., Van Camp G.; "Nonsyndromic hearing impairment is associated with a mutation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATC 33530 / G-37;
MEDLINE=5602346; PubMed=7569993;
MEDLINE=5602346; PubMed=7569993;
MEDLINE=5602346; PubMed=7569993;
Pleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fleischmann R.D., Manlar K.V., Sandusky W., Fuhmann J.L., Woldman J.F., Small K.V., Sandusky M., Fuhmann J.L., Nouyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13AFB8627773C4A5 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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01.FEB-1996 (Rel. 33, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical helicase MG018.
                                                                                                                                                                                                                         Nat. Genet. 20:194-197(1998).
-!- SIMILARITY: BELONGS TO THE DFNS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 AA
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TISSUE=Cochlea;
MEDLINE=98442658; PubMed=9771715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF073309; AAC69325.1; -.
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SEQUENCE 512 AA; 56630 MW;
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InterPro; IPR007677; DFNAS.
InterPro; IPR007681; Mobl.
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Best Local Similarity:
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SIGNAL
CHAIN
PEPTIDE
PEPTIDE
DISULFID
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CONFLICT
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B) (CgB) [Contains: GAWK
                                                                                                                                                                                                                                                                                                                                                                   sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-!- MISCELLANBOUS: IN M.PNBUMONIAE, A SINGLE ORF SPANS M.GENITALIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea,
Bovidae; Bovinae; Bos.
VCBI_TaxID=9913;
                                                                                       C.A. III;
by using random
                                                                                                                                                                              MG016, MG017 AND MG018.
-!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   000000
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Matches:
Conservative:
                              SEQUENCE OF 209-309 AND 371-471 FROM N.A. STRAIN=ATCC 33530 / G-37; MEDLINE=94075230; PubMed=8253680; Medreso S.N., Hu P.-C., Bott K.F., Hutchison "A survey of the Mycoplasma genitalium genome ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGI BOVIN STANDARD; PRT; 646 AA. P23369; 002707; 10.004-1991 (Rel. 20, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) peptide; Secretogranin I precursor (SgI) (Chromogranin peptide; Secretolytin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Adrenal chromaffin;
MEDLINE-91223091; PubMed-2025642;
Bauer J.W., Fischer-Colbrie R.;
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Query Match:
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DT 01-NO

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DT 16-NO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION OF SECRETOLYTIN.

MEDLINE=96184581; PubMed=8603705;

Strub J.M., Hubert P., Nullans G., Aunis D., Metz-Boutigue M.-H.;

Strub J.M., Eubert P., Nullans G., Aunis D., Metz-Boutigue M.-H.;

peptide (614-626), is correlated with peptide structure.";

FEBS Lett. 379:273-278(1996).

-I-FUNCTION: Secretogranin I is a neuroendocrine secretory granule protein, which may be the precursor for other biologically active peptides. The 16 pairs of basic AA distributed throughout its sequence may be used as proteolytic cleavage sites.

-I-FUNCTION: Secretolytin has antibacterial activity.

-I-SUBCELJULAR LOCATION: Neuroendocrine and endocrine secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Addenal chromaffin, MEDLINE=9526269; PubMed=7744058; Strub J.-M., Garcia-5ablone P., Lonning K., Taupenot L., Hubert P., Strub J.-M., Aunis D., Metz-Boutique M.-H.; Improcessing of chromogranin B in bovine adrenal medulla. Identification of secretolyth, the endogenous C-terminal fragment of Fesiques 614-626 with antibacterial activity."; Euchem. 229:356-368(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: O-glycosylated (Probable). SIMILARITY: Belongs to the chromogranin / secretogranin protein
                                                                                                                                                                                                                                                              ŏ
                                                                                                                  SEQUENCE FROM N.A.
TISSUB-Adrenal medulla;
TISSUB-Adrenal medulla;
TISSUB-Adrenal medulla;
TOS S.H., Kang Y.K.;
"Identification of the secretory vesicle membrane binding region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grandy D.K., Leduc R., Makam H., Flanagan T., Diliberto E.J., Thomas G., Civelli O., Viveros O.H.; Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
Primary structure of bovine chromogranin B deduced from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X55027; CAA38846.1; -.
EMBL; U88551; AAC48720.1; -.
EMBL; X55489; CAA39109.1; -.
EMBL; X55489; CAA39109.1; -.
EMBL; X55489; CAA39109.1; -.
EMBL; X55489; CAB39109.1; -.
EMBL; X55489; CAB0109.1; -.
EMBL; X55489; CAB0109.1; -.
EMBL; X55489; CAB0109.1; -.
EMBL; PS00422; GRANINS.1; 1.
EMBL; PS00423; GRANINS.2; 1.
Sulfation; Cleavage on pair of basic residues; Signal.
SIGNAL
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BY SIMILARITY.
SULFATION (POTENTIAL).
SULFATION (BY SIMILARITY).
N -> S (IN REF. 1).
N -> D (IN REF. 2).
                                                              Biochim. Biophys. Acta 1089:124-126(1991).
                                                                                                                                                                                                                                                                                          chromogranin B.";
FEBS Lett. 406:259-262(1997).
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 21-646 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Adrenal medulla;
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STARAIN-BUREL; TISSUE-Mammary gland;

WEDLINE=2238257; PubMed=12477932;

WEDLINE=2238257; PubMed=12477932;

WEDLINE=2238257; PubMed=12477932;

WEDLINE=2238257; PubMed=12477932;

WELLSTARE R.D., Collins F.S., Wegner L.H., Derge J.G., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Historia S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brapleton M., Soares M.B., Bonaldo M.F., Caramon R.D., Mullahy S.J., Brands S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Galve B.H., Wilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Allalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J. M., Marra M.A., T., Changel M.A., Robersation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-!- FUNCTION: Transcriptional regulator that acts as repressor or activator. Binds, in-vitro, to NF-E2 binding sites. Play important roles in coordinating transcription activation and repression by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/c;
MEDLINE=97042438; PubMed=8887638;
MEDLINE=97042438; PubMed=8887638;
Yoyake T., Itoh K., Motohashi H., Hayashi N., Hoshino H., Nishizawa M., Yamamoto M., Igarashi K.;
"Bach proteins belong to a novel family of BTB-basic leucine zipper transcription factors that interact with MafK and regulate transcription through the NF-EZ site.";
Mol. Cell. Biol. 16:6083-6095(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fukaryota; Marazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Transcription regulator protein BACH1 (BTB and CNC homolog 1).
         (IN REF. 3).
                           T -> M (IN REF. 2).
H -> R (IN REF. 2).
F -> R (IN REF. 2).
H -> L (IN REF. 3).
M -> V (IN REF. 3).
420DB1178FD9E415 CRC64;
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Matches:
Conservative:
Mismatches:
         FRSPRAS
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93
181
261
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646 AA;
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Query Match:
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                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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15-JUL-1998
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SEQUENCE
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BAC1 MOU
P97302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NR GO; GO:0005634; C:nucleus; IDA.

CO; GO:0005515; P:protein binding; IPI.

CO; GO:000515; P:protein binding; IPI.

CO; GO:000515; P:protein binding; IPI.

CO; GO:0003500; F:transcription factor activity; IDA.

CO; GO:000355; P:regulation of transcription, DNA-dependent; IDA.

R GO; GO:0006315; P:ROGO110; BIB POZ.

R InterPro; IPR00210; BIB POZ.

R InterPro; IPR00411; LeuZip Jun.

R Pfam; PF00415; IPR04821; TF_DZIP.

R Pfam; PF00404; LEUZIPPRJUN.

R PRINTS; PR00043; LEUZIPPRJUN.

R SWART; SM00325; BIB; 1.
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PROSITE; PSSO217; BZIP; 1.
PROSITE; PSO0065; BZIP BASIC; 1.
Transcription regulation; Activator; Repressor; DNA-binding;
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Cystobacterineae; Myxococcaceae; Myxococcus.
-!- SUBUNIT: Heterodimer of BACH1 and MAFK.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- TISSUB SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Belongs to the DZIP family. CNC subfamily.
-!- SIMILARITY: Contains 1 BTB/POZ domain.
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BASIC MOTIF.
LEUCINE-ZIPPER.
CE2DE606B05F6E32 CRC64;
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Mismatches:
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15-DEC-1998 (Rel. 37, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
DNA gyrase subunit B (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   815 AA.
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Matches:
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STRAIN=ER-15;
MEDLINE=98304088; PubMed=9639935;
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D86603; BAA13137.1; -.
EMBL; BC057894; AAH57894.1; -.
HSSP; B34707; ISKN.
TRANSFAC; T04793; -.
MGD; MGI:894680; Bach1.
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739 AA;
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033367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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TOP2 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Paitan Y., Boulton N., Ron E.Z., Rosenberg E., Orr E.;
"Molecular analysis of the DNA gyrB gene from Myxococcus xanthus.";
Microblology 144:1647(1998).

-: FUNCTION: DNA gyrase negatively supercoils closed circular double-
stranded DNA in an ATP-dependent manner and also catalyzes the
interconversion of other topological isomers of double-stranded
DNA rings, including catenanes and knotted rings.

-: CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
of double-stranded DNA:
- SUBUNIT: Made up of two chains: The A chain is responsible for DNA
breakage and rejoining; the B chain catalyzes ATP hydrolysis. The
enzyme forms an A2B2 tetramer.
-: SIMILARITY: Belongs to the type II topoisomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical helicase MG018/MG017/MG016 homolog (D12_orf1030)
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PROSITE; PS00177; TOPOISOMERASE II; 1.
TOPOISOMERASE; ISOMERASE; ISOMERASE; ISOMERASE; REPAINDING.
SEQUENCE 815 AA; 89636 MW; 3867685FBB805B32 CRC64;
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STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR002288; DNA_gyraseB_C.
InterPro; IPR0001241; DNA_typoisoII.
InterPro; IPR001241; DNA_typoisoII.
InterPro; IPR006171; Toprim dom.
Pfam; PF00204; DNA_gyraseB_C; I.
Pfam; PF00204; DNA_gyraseB_C; I.
Pfam; PF07518; HATPase_C; I.
Pfam; PF07518; Toprim; I.
PRINTS; PR00481; TP12PAMILY.
Pr0DOm; PD149633; DNA_gyraseB_C; I.
SMART; SM00433; TOP2C; I.
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P75093;
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'Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of a DNA Topoisomerase II cDNA from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein, Helicase, ATP-binding, Complete proteome. NP_BIND 603 610 ATP (POTENTIAL).
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                                                                -!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
-!- SIMILARITY: TO M.GENITALIUM MG016, MG017 AND MG018.
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DEAQ BOX. ..... 7272E2B162AF1737 CRC64;
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                       pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996)
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STRAIN-cv. Columbia, and cv. Kas-1;
MEDLINE=95140639; PubMed=7838729;
                                                                                                                                                                                                                                                                                                                                   | PIR; $73460; $73460. |
| ENERPLYO. | IRROULDION | |
| INTERPLYO. | IPROUNDESO. |
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| INTERPLYO. | IPROUNDESO. | SNRZ N. |
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| INTERPLYO. | IPROUNDESO. | INTERPLYO. |
| Pfam; PFOOL76; SNR2 N; I. |
| Pfam; PFOOL76; SNR2 N; I. |
| SNART; SNO0487; DEXDC: | 1. |
| SNART; SNO0480; HELICC; | 1. |
| SNART; SNO0490; HELICC; | 1. |
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STRAIN-cv. Columbia;
MEDLINE=95148754; PubMed=7846176;
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The prolification in Arabidopsis thaliana, ', R. Wicletc Acids Res. 22:5729-5736(1994).

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US-09-270-437D-5 (1-1708) x TOP2\_ARATH (1-1473)

Search completed: July 13, 2004, 12:31:31 Job time : 31.5 secs

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Sequence 348, App
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Sequence 446, App
Sequence 449, App
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Sequence 1116, App
Sequence 1114, App
Sequence 1111, App
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Sequence
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| Sequence 500, Application US/10313986
| Publication No. US20030236209A1
| GENERAL INFORMATION:
| APPLICANT: Pred M. Andria
| APPLICANT: Read Y. Sethin No. APPLICANT: Read Y. Tongtong
| APPLICANT: Read Y. Tongtong
| APPLICANT: Read Y. Tongtong
| TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TILLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
| FILE REFERENCE: 210121.455C19
| CURRENT APPLICATION NUMBER: US/10/313,986
| CURRENT FILING DAIE: 2002-12-04
| NUMBER OF SEQ ID NOS: 560
| SOFTWARE FEBRESCE FEBRESCE FOR Windows Version 4.0
             US-09-873-637-2
US-09-873-637-2
US-09-873-637-2
US-09-860-7165-348
US-09-897-778-446
US-09-897-778-446
US-09-897-778-449
US-09-897-778-449
US-10-107-982-449
US-10-107-982-449
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US-10-107-982-4427
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-MUSGOZO0437/runat_13072004_121924_9724/app_query.fasta_1.1863
-DE-CGDZ_1/USFTO_spool p/USGO370437/runat_13072004_IRTN=blosum62
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62
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-MAXIEN=200000000 -USER=USGO377_9 CGN 1 1.130 @runat 13072004_121924_9724
-NCPU=6 -ICUPAT - NORM= -LARGEQUERY NORG - SORD - WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NRW_PUB_Pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_Pep:*
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| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                    protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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QY         986 ATGGTTATCATCACGGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGC 1045	Qy         1166 TTGCAGAATTTGACGGCAGCTGAGGTGGTAGTACCAAGACCCCTGATGAGAAC 1225	Qy         1286 ATCCGAGGACATCCTGGCCCAGGTTAAGCAGCATCAGAGGGACAGGACAGGCC 1345           Db         553 IleArgAspileLeuAlaGinValLysGlnGlnHisGlnLysGlyGlnSerAsnGlnAla 572           Qy         1346 CAGGCACGGAGGAAG 1360           Db         573 GlnAlaArgArgLys 577	RESULT 2 US-09-873-637-2 IS-09-873-637-2  Sequence 2, Application US/09873637 Factor No. US20020061543A1 GENERAL INFORMATION: TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN TITLE OF INVENTION: (CED. RED. AND THE MINGRED SECTION OF SECTION OF THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN	FILE REFERENCE: 960296.95131 CURRENT APPLICATION NUMBER: US/09/873,637 CURRENT FILING DATE: 2001-06-04 NUMBER OF SEQ ID NOS: 46 SOFTWARE: Patentin Ver. 2.0 I ENGTH: 577 TYPE: PRT	CRGANISM: Mus musculus   CRGANISM: Mus musculus   CS-09-873-637-2   Alignment Scores:   5.91e-167   Length:   S77   Scores:   2208.00   Matches:   438   Percent Similarity:   98.65%   Conservative:   1   Best Local Similarity:   98.43%   Mismatches:   4   Gaps:   1.00%   Indexis:   2   DBs:   1.00%		0y         92 TACATCCCCGATGAGCACAGGACCTGAGAATGGCCCCAGGGGGCCTTTGGC 151           bb         153 TYFI1eProAspGluGlnIleThrGlnGlyProGluAsmGlyArgArgArgGlyGlyPheGly 172           0y         152 TCTCGGGGTCAGCCCGCCAGGGCTCACCTGTGGCAGGGGGCCCCAGCCAAGCAG 211           Db         173 SerArgGlyGlnProArgGlnGlySerProValAlaAlaGlyAlaProAlaLySGlnGln 192           0y         212 CAAGTGGACTCCCCTTCGGCTCCTGGTGCCCACCCAGTATTGGC 271           Db         193 ProValAsplleProLeuArgLeuLeuValProThrGlnThrVyAlaIleIleIl	iss Fiovainaprieffoneumigheumeuvaiffoimfoimfyvaleiyhtalleuleury
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Patent No. US20020052329A1

Sequence 348, Application US/09735705

Patent No. US20020052329A1

GENERAL INFORMATION:

APPLICANT: Fan, Liqun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Ailun
APPLICANT: Wang, Ailun
APPLICANT: Wang, Ailun
APPLICANT: Ranger, Nell
APPLICANT: Ranger, Nell
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
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{\tt AspIleLysPheThrGluGluIleProLeuLysIleLeuAlaHisAsnAsnPheValGly~289}
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                                    ATCACCATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTG
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Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
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Matches:
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CURRENT APPLICATION NUMBER: US/09/850,716A CURRENT FILING DATE: 2001-05-07 NUMBER OF SEQ ID NOS: 440 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 348 LENGTH: 579 TYPE: PRI
                                                                                                                                                                                                    1.26e-121
1639.00
83.89%
74.17%
52.70%
                                                                                                                             ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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LysGlnLysProCysAspLeuProLeuArgLeuLeuValProThrGlnPheValGlyAla
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                                                                                                        ATTATTGGCAAGGAGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATA
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                                  CGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCC
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                                       ATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGCCATCATCGGCAAGAAGGGCCAG
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Sequence 348, Application US/09897778

Patent No. US20020147143A1

SGENERAL INPORMATION:
APPLICANT: Ward, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Garter, Thomas S.
APPLICANT: Garter, Darrick
APPLICANT: Maranabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: ComPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPRENCE: 210121.455C16
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOSPIWARE: FastSEQ for Windows Version 4.0
SEG ID NO 348
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Matches:
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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-897-778-348
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Db 190 LysGlnLysProCysAspLeuProLeuArgLeuLeuValProThrGlnFheValGlyAla 209  Qy 263 ATTATTGGCAAGGGGGCCACCATCGCAACATCACAAAACAGAACCAGTCCAAGATA 322  Dh 210 [1611	323 GACGTOCATAGGAAGGAGGAGCTGAAAAAGCCATCAACACACCACC CACC	CCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAG 44	Qy 443 GACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGG 502	Oy 503 CGTCTCATTGGCAAGGAAGGAACCTGAAGAAGGTAGGAAGATACCGAGACAAAA 562  Db 290 ArgLeulleGlyLysGluGlyArgAsnLeuLysLyslieGluGlnAspThraspThriys 309	OY 563 ATCACCATCTCGTTGCAAGACCTTTACCAACCCTGAGGACCATCACTGG 622	Qy 623 AAGGGGCCATGGAGAATTGTTGCAGGGCCGAGCAGAAATAATGAAGAAAGGTTCGGGAG 682	Qy 683 GCCTATGAGAATGATGCTGCCATGAGCTCTCACCTGATCCTGGCCTGAAC 736 :::	Qy 737 CTGGCTGTAGGTCTTTTCCCAGCTTCATCCAGCGCAGCG	OY 788 CCCAGCAGCGTTACTGGGGCTGCTCCTATAGCTCCTTTATGCAGGTCCCGAGCAGGAG 847	OY 848 AIGGIGCAGGIGTITAICCCGGCCAGCAGGGGGCGCCAICAICGGCAGAAGAGGGGCAG 907	Qy 908 CACAICAAACAGCICTCCCGGTITGCCAGCGCCTCCATCAAGAITGCACCCCCAAACA 967	Oy 968 CCTGACTCCAAAGTTGGTTATCATCACTGGACGGCCGAAGGCCCAATTCAAGGCT 1027	Qy 1028 CAGGGAAGAATCTATGGCAAACTCAAGGAGGAAGAACTTCTTTGGTCCCAAGGAAGTG 1087	Qy 1088 AAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT 1147	Qy 1148 GGAAAAACGGTGAACCAGTTGCAGAATTTGACGGCAGCTGAGGTAGTACCAAGAGAC 1207 	Qy 1208 CAGACCCTGATGAGAACGACCATCGTGAAAATCATCGGACATTTCTATGCCAGT 1267	Qy         1268         CAGATGGCTCAAGGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAG         1324
Db 467 GlnGlyArgileTyrGlyDysIleLysGluGluAsnPheValSerProLysGluGluVal 486 Qy 1088 AACTGAAGACCCACATACGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT 1147 Db 487 LysLeuGluAlaiisIleArgValProSerPhaAlaAlaGlyArgal11eGyLysGly, 506		Qy 1208 CAGACCCCTGATGAGACGACCAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGT 1267	Qy 1268 CAGATGGCTCAACGGAAGATCCGGACATCCTGGCCCCAGGTTAAGCAGCAGCATCAG 1324	Qy 1325 AAGGACACAGTAACCAGGCCCAGGAGGAAG 1360	RESULT 6 US-09-897-778-446 Sequence 446, Application US/09897778 ; Parent No. US2002014714A1	; GENERAL INFORMATION: ; APPLICANT: Wang, Tongtong ; APPLICANT: Warnerfis, Margarita ; APPLICANT: Panger Gary P	HPPLICANT: Vedvick, Thomas S. HPPLICANT: Vedvick, Thomas S. HPPLICANT: Carter, Darrick HPPLICANT: Watanabe, Yoshihiro HPPLICANT: Henderson Pohert a	APPLICANT: Peckham, David W. APPLICANT: Penger, Neil TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DISCHOOLE OF TIME CANDED.	FILE REFERENCE: 210121.455C16 CURRENT APPLICATION NUMBER: US/09/897,778 CURRENT FILING DATE: 2001-06-28 NUMBER OF SEC 17 NOS. 457	SOTTWARE: FactSEQ for Windows Version 4.0 SEQ ID NO 446 LENGIN 579 TYPE: PRT	; ORGANISM: Homo sapiens US-09-897-778-446	Pred. No.: 1.26e-121 Length: 579 Score: 1639.00 Matches: 336 Percent Similarity: 83.89\$ Conservative: 44 Best Local Sinilarity: 74.17\$ Mismatches: 57	52.70% Indels: 9 Gaps: 708) v HG_00_807_700_446 (1_670)	OY 32 CGGGAGCCATCATGAAGTGCACACAGTTGCAGAACCATGCCCTGAAGGTCTCC 91	14	143 GGCTTTGGGGGTCAGCCCGGCCAGGGCTCACCTGTGGCAGGGGGGCCCCAGGC 20  173 GJCTTTGGGGGTCAGCCCGCCAGGGCTCACCTGTGGCAGGGGGGCCCCAGGC 20  173 GJCTTGGTAGTAAAGGAAAGGAAAGGAAAGGAAAGGAAAG	203 AAGCAGCAGCAAGTGGACATCCCCCTTCGGCTCCTGGTGCCCACTATGTGGGTGCC 26

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CGTCTCATTGGCAAGGAAGGACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAA
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US-10-007-700-348
Sequence 348, Application US/10007700
Sequence 348, Application US/10007700
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Li, Samual X.
APPLICANT: Handerson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNOWILL, Patricia D.
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US-09-897-778-449

Sequence 449, Application US/09897778

Sequence 449, Application US/09897778

Sequence 449, Application US/09897778

Sequence 449, Application US/09897778

Septicant: Wang, Tongtong

APPLICANT: Marnerakis, Margarita

APPLICANT: Panger, Gary R.

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick

APPLICANT: Wadanabe, Yoshhiro

APPLICANT: Henderson, Robert A.

APPLICANT: Peckham, David W.

APPLICANT: Peckham, David W.

APPLICANT: Peckham, David W.

APPLICANT: Pinvention: AND Diagnosis OF LUNG CANCER

TITLE OF INVENTION: COMPOSITIONS AND MATHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

TITLE REFERENCE: 210121.455C16

CURRENT FILING DATE: 2001-06-28

NUMBER OF SEQ ID NOS: 467

SEQ ID NO 449
  AAGGGA---CAGAGTAACCAGGCCCAGGCACGGAGGAAG 1360
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              Length:
Matches:
Conservative:
Mismatches:
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83.89%
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52.70%
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CRGANISM: Homo sapiens
US-09-897-778-449
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Best Local Similarity:
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|ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu 406
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390 ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu
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Li, Samual X.
Kalos, Machael D.
Henderson, Robert A.
MONeill, Patricia D.
Fanger, Marc W.
Durham, Margarita
Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
Matamabe, Yoshihiro
Peckman, David W.
Cai, Feng
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                                                                                                  APPLICANT: Cai, Feng
APPLICANT: Cai, Feng
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT APPLICATION NUMBER: 201-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 348
LENGTH: 579
                                                                                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                  Length:
Fanger, Neil
Retter, Marc W.
Durham, Margarita
Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
Watanabe, Yoshihiro
Peckman, David W.
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1639.00
83.89%
74.17%
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Best Local Similarity:
Query Match:
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ORGANISM: Homo
US-10-007-700-348
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                                                                                                                                                                                                                                                                                                407 ThrValHisLeuPheileProAlaLeuSerValGlyAlaIleIleGlyLysGlnGlyGln 426
                                                                                                                                                                                                    908 CACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACA 967
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                                                         CCCAGCAGCGTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAG
                                                                             |||||||::::::|||
390 ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu
                                                                                                                                                                                                                                                                                                                                                                        467 GlnGlyArgIleTyrGlyLysIleLysGluGluAsnPheValSerProLysGluGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND DAGMOSIS OF LUNG CANCER
FILE REPRENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FASUSEQ FOR WINGOWS Version 4.0
SEQ ID NO 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGGGA---CAGAGTAACCAGGCCCCAGGCACGGAAG 1360
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Retter, Marc W.
Durham, Margarita
Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
Watanabe, Yoshihiro
Peckman, David W.
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APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Li, Samual X.
APPLICANT: Rios, Michael D.
APPLICANT: Roles, Michael D.
APPLICANT: Moneill, Patricia D.
APPLICANT: Moneill, Patricia D.
APPLICANT: Retter, Marc W.
APPLICANT: Parger, Wali
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APPLICANT: Parger, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Peckman, Darick
APPLICANT: Peckman, David W.
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APPLICANT: Carter, Darrick
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LysGlyAsnValGluThrCysAlaLysAlaGluGluGluIleMetLysLysIleArgGlu 349
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LysGlnLysProCysAspLeuProLeuArgLeuLeuValProThrGlnPheValGlyAla 209
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|ArgGlnAlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLysValAla 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAG 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGAAATAATGAAGAAAGTTCGGGAG
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                       THE THERAPY
                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Foy, Teresa M.
TITE OF INVENTION: COMPOSITIONS AND METHODS FOR TITE. OF INVENTION: AND DIAGNOSIS OF LUNG CANCE; FILE REFERENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE FEASTSEQ for Windows Version 4.0
LENGTH: 579
                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                           1.26e-121
1639.00
83.89%
74.17%
52.70%
                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-700-446
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Percent Similarity:
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DB:
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Pred. No.:
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Db 407 ThrValHisLeuPheIleProAlaLeuSerValGlyAlaIleIleGlyLysGlnGlyGln 426  Qy 908 CACATCAAACAGTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCCGGAAACA 967	447 ProAspAlaLysValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAla 1028 CAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTG	467 GlnGlyArgileTyrGlyLysileLysGluGluAsnPheValSerProLysGluGluVal	1088 AMACIOGAGANCCACATACGIGIGCCAGCAICAGCAGCGGGTCGGCGGGTCATIGGCAAAGGT 	1148	Qy .1208 CAGACCCTGATGAGAACGACCAGGTCATGGTGAAATCATGGGAGATTTCTATGCCAGT 1267	Qy 1268 CAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAG 1324	Qy 1325 AAGGGACAGAGTAACCAGGCACGAGGAGGAAG 1360 	RESULT 11 US-10-117-982-348 ; Sequence 348, Application US/10117982 ; Publication No. US20030138438A1	; GENERAL INFORMATION: ; APPLICANT: FOY, Teresa M. ; APPLICANT: Fanger, Gary R. ; APPLICANT: Vedvick, Thomas S.	; APPLICANT: Carter, Darrick ; APPLICANT: Watanabe, Yoshihiro ; APPLICANT: Henderson, Robert A. ; APPLICANT: Kalos, Michael D.		; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER ; FILE REFERENCE: 210121.455018 ; CURRENT APPLICATION NUMBER: US/10/117,982	; CURRENT Filing DATE: 2002-04-05; NUMBER OF SEQ ID NOS: 484; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 348	LENGTH: 579 	1.26e-121 Length: 1639.00 Matches:	Percent Similarity: 83.89% Conservative: 44  Best Local Similarity: 74.17% Mismatches: 57  Ouery Match: 52.70% Indels: 16  DB: 14 Gaps: 9	US-09-270-437D-5 (1-1708) x US-10-117-982-348 (1-579)
-121 Length:	Secret Similarity: 1539.00 Marches: 336 Percret Similarity: 83.89% Conservative: 44 Pest Local Similarity: 74.17% Mismatches: 57 Query Match: 52.70% Indels: 16 DB: 9	US-09-270-437D-5 (1-1708) x US-10-007-700-449 (1-579)	Qy 32 CGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCC 91	OY 92 TACATCCCGATGAGCAGATAGCACAGGGACCTGAGAATGGGGCGCGAGGG 142	Qy 143 GGCTTTGGCTCTCGGGGTCAGCCCGCCAGGGCTCACCTGTGGCAGGGGGCCCCAGCC 202	Oy 203 AAGCAGCAGCAAGTGGACATCCCCCTTCGGCTCCTGGTGCCCACCAGTATGTGGGGCC 262	CAAGATA         rLysile	Oy 323 GACGTGCATAGGAAGGAGAACGCAGGTGCAGAAAAAGCCATCAGTGGACTCCACC 382 	Qy 383 CCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAG 442	OY 443 GACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGG 502	Qy       503 CGTCTCATTGGCAAGGAAGGAACCTGAAGAAAGGTAGGCAAGATACCGAGACAAAA 562         LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 563 ATCACCATCTCCTGGTAGGAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGG 622	Qy 623 AAGGGGCCATCGAGAATTGTTGCAGGCCGAGCAGGAAATAATGAAGAAAGTTCGGGAG 682	Oy 683 GCCTATGAGAATGATGGCTGCCATGAGCTCTCACCTGATCCCTGGCCTGAAC 736 :::	Oy 737 CTGGCTGCTGTAGGTCTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCT 787	Oy 788 CCCAGCAGCGTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGG 847	Qy 848 atggtgcaggtgttatcccgcccaggcagtggcccatcatcgccaagaagggcag 907

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GGAAAAACGGTGAACCAGTTGCAGAATTTGACGGCAGCTGAGGTGGTAGTACCAAGAGAC 1207
                                                                                                                        CAGACCCCTGATGAGGACCAGGTCATCGTGAAATCATCGGACATTTCTATGCCAGT 1267
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                                                                                                                                          CGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCC
CAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAG----CAGCATCAG
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                                                                           GlyLysThrValAsnGluLeuGlnAsnLeuSerSerAlaGluValValValValProArgAsp
                                                                                                                                                                                                                                                                                                                                           Sequence 446, Application US/10117982

Publication No. US20030138438A1

GENERAL INFORMATION:
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Vactor, Darrick
APPLICANT: Watanabe, Yoshithiro
APPLICANT: Watanabe, Yoshithiro
APPLICANT: Mariale, Barbara
APPLICANT: Menicle, Barbara
APPLICANT: Menicle, Barbara
APPLICANT: Fan, Liquu
APPLICAN
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LysalaLeuGlnSerGlyProProGlnSerArgArgLys 579
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-10-117-982-446
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Oy 1325 AAGGGACAGAGTAACCAGGCCCAGGCAGGAAGAA 1360  Db 567 LyshlaLeuGlnSerGlyProProGlnSerArgArgLys 579  RESULT 13 US-10-117-982-449 ; Sequence 449, Application US/10117982 ; Sequence 449, Application US/10117982 ; Publicare ion No. US20030138438A1 ; APPLICANT: Foy, Teresa M. ; APPLICANT: Foy, Teresa M. ; APPLICANT: Garter, Darrick ; APPLICANT: Wedvick, Thomas S. ; APPLICANT: Wearnabe, Yoshihiro ; APPLICANT: Marchael D. ; APPLICANT: Marchael D. ; APPLICANT: Marchael D. ; APPLICANT: Marchael D. ; APPLICANT: Mang, Tongtong ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ; TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER ; FILE REPERENCE: 21012.455ClB ; CURRENT APPLICATION NUMBER: US/10/117,982 ; UNDBER OF SEQ ID NOS: 484 ; SOFTWARES FastSEQ for Windows Version 4.0 ; SEQ ID NO 449 ; SEQ ID NO 449 ; TYPE: RA	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Cuery Match: A. 174	08-09-270-437D-5 (1-1708) x US-10-117-982-449 (1-579)           09         32 CGGCGGACCATCATGAAGCTCAAAGCTCACAGTTGCAAAGGTCTCC 91           133 ArgOlnAlaLeuAspLyeLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLysValAla 152           09         92 TACATCCCCAATGACAATAACACAGCGACACAGTGCGCGAGGGCCGAGGGCCCAGGGCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGGCCCCAGGCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCAGGGCCCCCC
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APPLICANT: Kalos, Michael D.
APPLICANT: Mericle, Barbara
APPLICANT: Spies, Gregory A.
APPLICANT: Spies, Gregory A.
APPLICANT: Fan, Liquo
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITION OF LUNG CANCER
FILE REFERENCE: 210121.455C18
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 494
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 579
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Matches:
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ORGANISM: Homo sapiens
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                                                                                                                                         SerTyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleFroGlyLeuAsn 369
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                                                                                            CACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACA
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     270 AspileLysPheThrGluGluIleProLeuLysIleLeuAlaHisAsnAsnPheValGly
                                                           ATCACCATCTCCTCGTTGCAAGACCTTACCAACCCTGAGGAGGACCATCACTGTG
                                                                    GCCTATGAGAATGAGCTGCCATGAGC-----TCTCACCTGATCCTGGCCTGAAC
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                                  CGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAA
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|VsAlaLeuGlnSerGlyProProGlnSerArgArgLys 579
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US-10-117-982-480
Squence 480, Application US/10117982
Publication No. US20030138438A1
GENERAL INFORMATION:
APPLICANT: Foy, Teresa M.
APPLICANT: Foy, Teresa M.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
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Percent Similarity: 83.89\$ Conservative: 44  Best Local Similarity: 74.17\$ Mismatches: 57  Query Match: 52.70\$ Indels: 16  DB: 15  US-09-270-437D-5 (1-1708) x US-10-313-986-348 (1-579)	Qy 32 CGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCC	Qy 92 TACATCCCCGATGAGCAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGG	Oy 143 GGCTTTGGCTCTCGGGGTCAGCCCGCCAGGGCTCACCTGTGGCAGGGGGGCCCCAGCC	Qy 203 AAGCAGCAAGTAGACATCCCCCTTCGGCTGCTGGTGCCCACCCA	Qy 263 ATTATTGGCAAGAGGGCCACCATCGCAACATCACAAACAGACCCAGTCCAAGATA	Qy 323 Db 230	Oy 383 CCTGAGGGCTGCTCCTCGGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAG	Qy         443 GACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGG	Qy         503 CGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAGGTAGGAAGAACAAAA	Qy         563 ATCACCATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGCACCATCACTGTG	330	Oy oss occurrences	Qy 737 CTGGCTGCTGTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCT	SAGC	Qy 848 AIGGIGCAGGIGITIAICCCGCCCAGGCAGGGGCGCCATCAICGCAAGAAGGGGCAGGGGGGGGGG	Qy 908 CACATCAAACAGCTCTCCCGGATTTGCCAGCGCCTCCATCAAGATTGCACCACCGGAACA	968 CCTGACTCCAAAGTTC
:::	788 CCCAGCAGCGTTACTGGGGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAG 847	848 ATGGTGCAGGTGTTTATCCCCGCCCAGCAGTGGGCGCCATCATCGGCAAGAAGGGGCAG 907	908 CACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACA 967	968 CCTGACTCCAAAGTTGGTAATCATCACAGGACCGCCAGAGGCCCAATTCAAGGCT 1027	1028 CAGGGAAGAATCTAIGGCAAACTCAAGGAGGAAGAACTTCTTIGGTCCCAAGGAGGAGGAG 1087 	1088 AAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCGGGTCATTGGCAAAGGT 1147 	1148 GGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTGGTACCAAGAGAC 1207	1208 CAGACCCCIGAIGAGGACCACCAGGICAICGIGAAAAICAICGGACAITITCIAIGCGGI 1267 	1268 CAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAG 1324	1325 AAGGGACAGAGTAACCAGGCCCAGGCACGAAGAG 1360 	RESULT 15 US-10-313-986-348 ; Sequence 348, Application US/10313986 ; Publication No. US20030236209A1 : GENERAL THERREAL	LICANT FOY, Teresa M. LICANT POY, Teresa M. LICANT Watanabe Vochihiro	LICANT: Reed, Steven G. LICANT: Read, Tongtong LICANT: Wang, Tongtong LE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	FILE REPRENCE: 210121.455C19 ; CURRENT APPLICATION NUMBER: US/10/313,986 ; CURRENT FILING DATE: 2002-12-04	DER OF SEX ID NOS: SeV TWARE: FastSEQ for Windows Version 4.0 ID NO 348 NGTH: 579	lires: FKI ORGANISM: Homo sapiens L0-313-986-348	Alignment Scores: 1.26e-121 Length: 579 Score: 1639.00 Matches: 336

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1208 CAGACCCTGATGAGAACGACGACATGTGAAATCATCGGACATTTCTATGCCAGT 1267
527 GInThrProAspGluAsnAspGlnValValValValIssIleThrGlyHisPheTyrAlaCys 546
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                                                                                                                           1148 GGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGGGGTGGTAGTACCAAGAGAC 1207
                                         507 GlyLysThrValAsnGluLeuGlnAsnLeuSerSerAlaGluValValValValProArgAsp 526
447 ProAspAlaLysValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAla 466
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Sequence 25951, A
Sequence 550, Ap
Sequence 650, Ap
Sequence 650, Appli
Sequence 7, Appli
Sequence 64, Appli
Sequence 19, Appli
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US-09-261-855-2
Sequence 2, Application US/09261855A
Sequence 2, Application US/09261855A
Sequence 2, Application US/09261855A
September 100. 6255055
GENERAL INFORMATION:
APPLICANT: ROSS, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CPD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960296.95131
CURRENT FILING DATE: 1999-03-03
SOFTWARRE: PATCHIN VET: 2.0
SOFTWARRE: PATCHIN VET: 2.0
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US-09-261-855-32

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US-09-261-855-12

US-09-261-855-13

US-09-261-855-13

US-09-252-991A-29417

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US-09-093-227-2

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; ORGANISM: Mus musculus
US-09-261-855-2
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14: /Cgn2_6/ptodatca/2/iaa/6B_COMB.pep:*
15: /Cgn2_6/ptodatca/2/iaa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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AAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGGTTGC 394
                                                                                                                                                                                                                                                                                                334 GluksnCysCysArgAlaGluGlnGluIleMetLysLysValArgGluAlaTyrGluAsn 353
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US-09-261-855-18
US-09-261-855-18
Sequence 18, Application US/09261855A
Sequence 18, Application US/09261855A
September 100. 6255055
GENERAL INFORMATION:
APPLICANT: ROSS, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: 18/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARRE: Patentin Ver. 2.0
SOFTWARRE: Patentin Ver. 2.0
                                                                                                           GCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGC
                                                                                                                                                                     AAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATCACCATCTCC
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Matches:
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US-09-261-855-20
; Sequence 20, Application US/09261855A
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CRGANISM: Mus musculus
US-09-261-855-18
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Best Local Similarity:
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Pred. No.:
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1103 ATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGTGGAAAACGGTGAAG 1162
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GENERAL INFORMATION:
APPLICATIVE, ROSS, Jeffrey
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE REPRENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
SEQ ID NOS: 46
SOFTWARE: PATCHIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09261855A
Patent No. 6255055
FIGHERAL INFORMATION:
APPLICANT: ROSS, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CPL-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960296, 95131
CURRENT APPLICATION NUMBER: US/09/261,855A
NUMBER OF SEQ ID NOS: 46
SOFTWARR: PATENTIN VET. 2.0
SOFTWARR: PATENTIN VET. 2.0
SOFTWARR: PATENTIN VET. 2.0
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ORGANISM: Mus musculus
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Query Match:
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Best Local Similarity:
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ORGANISM: Homo sapiens
                 US-09-643-597-176
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 21 AsnileThrLysGlnThrGlnSerLysIleAspValHisArgLysGluAsnAlaGlyAla 40
                                                                                                                           SQUENCE 19, Application US/09261855A

Factor 19, Application US/09261855A

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: (CRD-BP)
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (CRD-BP) AND IS NUCLEIC ACID SEQUENCE
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
ILENGTH: 47
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Raios, Michael D.
APPLICANT: Raios, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Cary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: McNeill, Particia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITION OF STORMARE: FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
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Mismatches:
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Matches:
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US-09-643-597-176
Sequence 176, Application US/09643597
Parent No. 6426072
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CORGANISM: Mus musculus
US-09-261-855-19
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chateanya S.
APPLICANT: Bangur, Chateanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Banger, Gary R.
APPLICANT: Wang, Aiun
APPLICANT: Weekly, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Menderson, Robert A.
APPLICANT: Moneill, Parricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CURRENT PILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOUTHWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
                Length:
Matches:
Conservative:
Mismatches:
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US-09-480-884A-176
Sequence 176, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
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; Sequence 348, Application US/09643597
; Patent No. 6426072
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, ORGANISM: Homo sapiens
US-09-643-597-348
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Best Local Similarity:
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Alignment Scores:
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Patent No. 6518256

GENERAL INFORMATION:
APPLICANT: Fan, Liqun
APPLICANT: Fanger, Cary R.
TITLE OF INVENTION: COMPOUNDS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE REPRENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: US/09/542,615A
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Ligun
APPLICANT: Fan, Ligun
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: DSCOFT OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-542-615A-176
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Falos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Hosken, Nancy
APPLICANT: Hanger, Gary R.
APPLICANT: Wang, Aiun
APPLICANT: Skeiky, Yasin A.W.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 200121.455C9
CURRENT APPLICATION NUMBER: 126/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
227 SerLysIleAspValHisArgLysGluAsnAlaGlyAlaAlaGluLys 242
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                                                                                                                                                                                                               APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Brangur, Cary R.
ITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
ITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C8
CURRENT FALLICA DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
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                                                                                                                                             Sequence 348, Application US/09542615A patent No. 6518256; GENERAL INFORMATION:
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US-09-542-615A-348
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CORGANISM: Homo sapiens
US-09-606-421B-176
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US-09-606-421B-176
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Query Match:
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Fatent NO. 62525055
GENERAL INFORMATION:
APPLICANT: ROSS, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REPERENCE: 960296.95131
                                                                                                                                                                                                                                            RESULT 12

US-09-606-421B-348

US-09-606-421B-348

Sequence 348, Application US/09606421B

Patent No. 6531315

GENERAL INPRMATION:
APPLICANT: Wang, Aigun
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Swels, Nach
APPLICANT: Swels, Nach
APPLICANT: Nang, Aigun
APPLICANT: Skelsky, Yasir A.W.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348

LENGTH: 279

LENGTH: 279

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         Length:
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Score: 36.00
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CORGANISM: Homo sapiens
US-09-606-421B-348
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US-09-261-855-21
Alignment Scores:
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| Sequence 24, Application US/09261855A
| Sequence 24, Application US/09261855A
| Patent No. 6255055
| General Investmanton:
| APPLICANT: Ross, Jeffrey
| TITLE OF INVENTION: (RD-BP) AND ITS NUCLEIC ACID SEQUENCE
| TITLE OF INVENTION: (RD-BP) AND ITS NUCLEIC ACID SEQUENCE
| TITLE OF INVENTION: (RD-BP) AND ITS NUCLEIC ACID SEQUENCE
| CURRENT PELICHON DATE: 1999-03-03
| NUMBER OF SEQ ID NOS: 46
| SEQ ID NOS: 46
| SEQ ID NO 24
| LENGTH: 48
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; Sequence 3, Application US/09261855A
; Patent No. 625505
; Patent No. 625505
; Patent No. 625505
; TITLE OF INVENTION: TE NO. 17 TITLE OF INVENTION: TE NO. 18 NO.
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Matches:
CURRENT APPLICATION NUMBER: US/09/261,855A CURRENT FILING DATE: 1999-03-03 NUMBER OF SEQ ID NOS: 46 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 21 LENGTH: 47 TYPE: PRT
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CRGANISM: Homo sapiens
US-09-261-855-24
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
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Pred. No.:

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Percent Similarity:
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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENCTH: 14
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-261-855-3
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Search completed: July 13, 2004, 12:36:38 Job time : 28 secs

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             Abp61968
Ada28217
Ada28218517
Adb74960
Ada28266
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ADA28438
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ABG21965
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WPI; 1999-551506/46.
N-PSDB; AAZ10617.
Mus musculus.
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AAY30649;
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                                                  Search time 82 Seconds (without alignments) 11770.516 Million cell updates/sec
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1 agggacgctgccgcaccgcc.....atttccttcaggttttaaaa 1708
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                    protein search, using frame_plus_n2p model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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2. geneseqp1990s:*

4. geneseqp2001s:*

5. geneseqp2001s:*

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vaccine; detection
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17-DEC-1999;
30-DEC-1999;
10-JAN-2000; 2
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               The present sequence represents a murine c-myc coding region determinant binding protein (CRD-BP). The presence or absence of a tumor can be determined by determining the levels of CRD-BP present in the suspect tissue, where the CRD-BP shields c-myc RNA from endonucleolytic attack and so prolongs its half-life. The methados are used for diagnossing presence or absence of a tumor in a buhnd, especially breast, colon and pancreatic cancer. They are also used to inhibit cancer cell growth
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                               AlaAlaProTyrSerSerPheMetGlnAlaProGluGluGluMetValGlnValPheIle
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GCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATC
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                                                                                   This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have eytostatic activity. The polypeptides and polymucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polymucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
                                 cancer
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          Isolated polypeptide comprising an immunogenic portion of a lung protein is used for detecting and monitoring progression of lung in a patient.
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                                                                                GCCTATGAGAATGATGTGGCTGCCATGAGC-----TCTCACCTGATCCCTGGCCTGAAC
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ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu 406
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                                             ATCACCATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGGACCATCACTGTG
                                                                                                      310 IleThr1leSerProLeuGlnGluLeuThrLeuTyrAsnProGluArgThr1leThrVal
                                                                                                                                                                                                     GCCTATGAGAATGAGCTGCCATGAGC----TCTCACCTGATCCCTGAGC
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                                CGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAA
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                                                                                                                                                                                                                                                                                                                                                    fusion
                                                                                                                                                                                                                                                                                                    The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, proteins, proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. AB448959 to AB449300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Henderson RA;
Fanger GR;
                                                                                                                                                                                                                                 tumor polypeptides, useful for immune response.
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MW, Marnerakis M,
oe Y, Peckham DW;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                             Claim 2; Page 365-367; 374pp; English
                                                                                                                                              Fanger N, Retter MW
Carter D, Watanabe
02-AUG-2000; 2000US-006430940.
21-AUG-2000; 2000US-00643597.
15-SEP-2000; 2000US-00662786.
9-SEP-2000; 2000US-00685696.
12-DEC-2000; 2000US-00735705.
07-MAY-2001; 2001US-00850716.
                                                                                                                                  YAW,
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N-PSDB; ABL49297.
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                                                                                                                                Wang A,
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Percent Similarity:
                                                                                                                             Wang T, Wang
Mcneill PD,
Vedvick TS,
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LysGlyAsnValGluThrCysAlaLysAlaGluGluGluIleMetLysLysIleArgGlu
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| ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu
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               GACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAAGCCATCAGTGTGCACTCCACC
                                                             CCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAG
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Retter MW, Marnerakis M,
Watanabe Y, Peckham DW;
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21-AUG-2000; 2000US-00643597.
15-SEP-2000; 2000US-00662786.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion
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                                                                                                                       Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor polypeptides, useful for treating immune response.
                                                                                               Human lung tumour L523S recombinant protein sequence SEQ ID NO:449
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Fanger GR;
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f, Peckham DW;
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Mcneill PD, Fanger N, Retter MW, N
Vedvick TS, Carter D, Watanabe Y,
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, 2000US-0068566.
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N-PSDB; ABL49299.
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12-DEC-2000; 07-MAY-2001; 2
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Mismatches: Indels:

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      74.178
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                                                                                         GlnValAlaGlnArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGlnGlnGln
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nger GR, Vedvick TS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; lung tumour; cytostatic; gene therapy; vaccine.
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Durham M, Fanger GR,
7, Cai F, Foy TM;
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| LysAlaLeuGlnSerGlyProProGlnSerArgArgLys
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Retter MW, D
Peckham DW,
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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Durham M, Fanger GR, Vedvick TS;
Cai F, Foy TM;
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                   CAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTG
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LysLeuGluhlaHisIleArgValProSerPheAlaAlaGlyArgValIleGlyLysGly
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|VsAlaLeuGlnSerGlyProProGlnSerArgArgLys
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Retter MW, D
Peckham DW,
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28-JUN-2001; 2001US-00897778.
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J, Watanabe Y,
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N-PSDB; ABQ92485.
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the polynucleotides, useful in pharmaceutical compositions such vaccines and as markers to indicate the presence of lung cancer.
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PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick
), Watanabe Y, Peckham DW, Cai F, Foy TM;
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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The present invention describes isolated human lung carcinoma polyuncleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polyuncleotide that hybridises to the oligonucleotide to a predecermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as marker to indicate the presence or absence of a cancer such as lung cancer. ABO92145 to ABO92486 and ABPG1866 to ABPG1992 represent sequences used in the exemplification of the present
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Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
Mcneill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
                                                                                                                             2000US-00480884.
2000US-00510376.
2000US-00542615.
                                                                    99US-00285479.
99US-00466396.
99US-00476496.
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2000US-00643597.
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                                                                                                                           10-JAN-2000; 22-FBB-2000; 28-JIN-2000; 28-JIN-2000; 21-AUG-2000; 21-AUG-2000; 21-AUG-2000; 29-OCT-2000; 29-OCT-2000; 20-OCT-2000; 20-OC
              18-MAR-1998;
27-JUL-1998;
22-DEC-1998;
02-APR-1999;
17-DEC-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                 12-DEC-2000;
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| LysAlaLeuGlnSerGlyProProGlnSerArgArgLys 579
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TyrileProAspGluThrAlaAlaGlnGlnAsnProLeuGlnGlnProArgGlyArgArg 172
                                                                                                                                                                       for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polymucleotide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; a sequence that hybridise to any of the nucleotide sequences under highly stringent conditions; a sequence that is at least 75 or 90% identical to the above nucleotide sequences; or degenerate variants of the above incleotide sequences; or degenerate variants of the above diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This is the amino acid sequence of a recombinant human lung tumour associated protein.
                                                                                                                                                 The invention describes isolated polynucleotides and polypeptides useful
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for diagnosing, cancer.
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New isolated polynucleotides and polypeptides useful preventing and/or treating cancer, particularly lung
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Mismatches:
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                                                                                        Claim 9; Page 285-287; 296pp; English.
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Mcneill PD,
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The invention describes isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polynucleotide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; at sequence that hybridise to any of the nucleotide sequences under highly stringent conditions; as sequence that is at least 75 or 90% identical to nucleotide sequences; or degenerate variants of the above nucleotide sequences; or degenerate variants of the above nucleotide sequences; or degenerate variants of the above nucleotide sequences. The composition and methods are useful in gene therapy and in vaccines. This is the amino acid sequence of a recombinant human lung tumour associated protein.
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PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick
), Watanabe Y, Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; lung cancer; gene therapy; vaccine; human; lung squamous cell carcinoma.
Recombinant human lung tumour protein L523S
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                                                                                                                                                                                    ADA28539 standard; protein; 579
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27-JUL-1998, 98US-00123912.
22-APK-1999, 99US-00221107.
02-APK-1999, 99US-00246479.
17-DEC-1999, 99US-00466396.
10-JAN-2000, 2000US-00480804.
22-FEB-2000, 2000US-00480804.
22-APK-2000, 2000US-006421.
22-AUG-2000, 2000US-0066421.
22-AUG-2000, 2000US-00663997.
15-SEP-2000, 2000US-00663997.
15-SEP-2000, 2000US-00663997.
15-DEC-2000, 2000US-0066396.
09-CCT-2000, 2000US-0066396.
15-DEC-2000, 2000US-0066396.
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                                                                                                                                                                                                                                                                                                                                        (first entry)
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09 1028 CCCCACTCCAAACTCCCAAACTCCCCCCCCCCCCCCCC	PA (CORI-) CORIXA CORP. XX XX PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA; PI Mcneill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS; PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM; XX
Scores   State   Sta	Db 407 ThrVaiHisLeuPheileProAlaLeuSerValGlyAlaileileGlyLySGlnGlyGln 426 Qy 908 CACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCGAAACA 967 Db 427 HislleLySGlnLeuSerArgPheAlaGlyAlaSerIleLysIleAlaProAlaGluAla 446

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The invention describes isolated polynuclectides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polynuclectide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; a sequence that hybridise to any of the nucleotide sequences under highly stringent conditions; a sequence that is at least 75 or 90% identical to the above nucleotide sequences, or degenerate variants of the above nucleotide sequences. The composition and methods are useful in diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This is the amino acid sequence encoded by a human lung tumour cDNA isolated from a lung squamous cell carcinoma that may be useful in the diagnosis and treatment of lung cancer and
                                                                               New isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer.
                                                                                                                                                         Example 2; Page 249-251; 296pp; English.
  2003-540798/51.
  WPI; 2003-540798
N-PSDB; ADA28437
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## 579 AA; Sequence

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Alignment Pred. No.	nent Scores: No.:	2.36e-144	Length:	579	
Percent Sim: Best Local Query Match DB:	ent Similarity: Local Similarity: 7 Match:	133.83.83.74.17.8 74.17.8 77.70.8	Matches: Conservative: Mismatches: Indels: Gaps:	ა 4 ს 11 თ ა 4 L ბი ა	
-60-SU	.270-437D-5 (1-1708)	08) x ADA28438	(1-579)		
λ	32 CGGGGAGC	CATCATGAAGCTGAA	TGGCCACCAGTTGGAG	GGGGGGGCATCATGAAGGTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCC 91	-
q	133 ArgGlnAla	: : : 	 nGlyPheGlnLeuGlu		52
λ̈	92 TACATCCC	TACATCCCCGATGAGCAGATAGCA-	-	CAGGGACCTGAGAATGGGCGCCGAGGG 14	142
qo	153 TyrilePr		  aGlnGlnAsnProLeu		172
ò	143 GGCTTTGG	CTCTCGGGGTCAGCC	CCGCCAGGGCTCACCT	SCCAGCC	202
<b>q</b> 0	173 GlyLeuGl	 yGlnArgGlySerSe	 	::: GlySerValser 1	83
ò	203 AAGCAGCA	GCAAGTGGAC	CCTTCGGCTCCTGGTGCCCA	CCCAGTATGTGGGTGCC	262
QQ	190 LysGlnLy	sProCysAspLeuPr	oLeuArgLeuLeuVal		60
ò	263 ATTATTGG	CAAGGAGGGG	CCACCATCCGCAACATCACA	CGCAACATCACAAAACAGACCCAGTCCAAGATA 323	22
qa	210 ileiledl	VLysGluGlyAlaTh	rileArgAsnileThr	elleglyLysgluglyAlaThrIleArgAsnIleThrLysglnThrGlnSerLysIle 22	5
6	323 GACGTGCA	TAGGAAGGAGAACGC	AGGTGCAGCTGAAAAA	CCATCAGTGTGCACTCCACC 3	82
qq	230 AspvalHi	sArgLysGluAsnAl	aGlyAlaAlaGluLys	AspValHisArgLysGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThr 24	<b>4</b>
ολ	383 CCTGAGGG	CTGCTCCTCCGCTTG	TAAGATGATCTTGGAG	CCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAG 44	42
qq	250 ProGluGL	 	ProgluglyThrSerAlaAlaCysLysSerIleLeuGlulleMetHisLysGluA	lagin 2	69
λŏ	443 GACACCAA	GACACCAAAACGGCTGACGAGGTTCCC	TCCCCTGAAGATCCTG		202
qq	270 AspileLy	SPheThrGluGluIl	eProbeutysileben		6.9
ò	503 CGTCTCAT	CATTGGCAAGGAAGGACGGAAC	GAACCTGAAGAAGGTAGAG	CAAGATACCGAGACAAAA 5	62
qq	290 Argheull	eGlyLysGluGlyAr	GASnLeuLysLysIle	ArgieulleGlyLysGluGlyArgAsnLeuLysLysIleGluGlnAspThrAspThrLys 30	60
δ	563 ATCACCAT	CTCCTCGTTGCAAGA	CCTTACCCTTTACAAC	ATCACCATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTG 62	622

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|ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                848 ATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGCCCATCATCGGCAAGAAGGGGCAG 907
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                                                                                                                         507 GlyLysThrValAsnGluLeuGlnAsnLeuSerSerAlaGluValValValValProArgAsp
                                                                                                                                                                                                          GCCTATGAGAATGATGTGGCTGCCATGAGC----TCTCACCTGATCCCTGGCCTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCAGCAGCGGTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAG
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|VsAlaLeuGlnSerGlyProProGlnSerArgArgLys
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ProGluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMetHisLysGluAlaGln 276
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                                            ArgLeulleGlyLysGluGlyArgAsnLeuLysLysIleGluGlnAspThrAspThrLys
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| ProSerAlaMetThr-----ProProTyrProGlnPheGluGlnSer---GluThrGlu
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                                                                                                                                                      317 IleThrIleSerProLeuGluGluLeuThrLeuTyrAsnProGluArgThrIleThrVal
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                                                                                                                                                                                                                                                                                                                                                The present invention describes human lung tumour proteins. Human lung activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polymucleotides, and can be used in vaccine production. Compositions proteins, T cell populations, or antigen presenting cells that express proteins, T cell populations, or antigen presenting cells that express stimulating an immune response. ABL48559 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                useful for treating
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Fanger GR;
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336
444
157
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                                                                                                                                                                                                                                                                               tumor polypeptides, immune response.
                                                                                                                                                                              J A, Skeiky YAW, Li SX, Kalos MD,
Fanger N, Retter MW, Marnerakis M,
Carter D, Watanabe Y, Peckham DW;
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Gaps:
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                                                                                                                                                                                                                                                                                                                        English.
                                   28-JUN-2000; 2000US-00606421.
02-AUG-2000; 2000US-00630940.
15-SEP-2000; 2000US-006643597.
15-SEP-2000; 2000US-00662786.
09-OCT-2000; 2000US-00685696.
12-DEC-2000; 2000US-00735705.
07-MAY-2001; 2001US-00850716.
                                                                                                                                                                                                                                                                                Polynucleotides encoding lung lung cancer or stimulating an
                                                                                                                                                                                                                                                                                                                        Claim 2; Page 354-355; 374pp;
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1639.00
83.89%
74.17%
52.70%
             2001WO-US021065
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N-PSDB; ABL49283.
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Query Match:
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Mcneill I
Vedvick 1
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The present invention describes isolated human lung carcinoma polypeptides (II). (I) and (II) have cytostatic polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the predecermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions. (I) contact used as marker to indicate the presence or absence of a cancer such as lung cancer. ABQ20145 to ABQ2146 and ABPG1866 to ABPG1992 represent sequences used in the exemplification of the present
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Retter MW, Durham M, Fanger GR, Vedvick TS;
Peckham DW, Cai F, Foy TM;
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                                  ID NO:427
                                                                                               cancer; lung tumour; cytostatic; gene therapy;
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                                  Human lung cancer associated protein sequence SEQ
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07-MAY-2001, 2001US-00850716.
28-JUN-2001, 2001US-00897778.
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Mcneill PD, Fanger N,
Carter D, Watanabe Y,
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              GACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAAGCCATCAGTGTGCACTCCACC
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The invention describes isolated polynuclectides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung deancer. A new isolated polynuclectide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above, at least 10 contiguous residues of the nucleotide sequences cited above; a sequence that hybridise to any of the nucleotide sequences cited above; the above nucleotide sequences that is at least 75 or 90% identical to the above nucleotide sequences; or degenerate variants of the above nucleotide sequences; or degenerate variants of the above diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This is the amino acid sequence of a recombinant human lung tumour associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for diagnosing, cancer.
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PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick
), Watanabe Y, Peckham DW, Cai F, Foy TM;
                                        AAGGGA---CAGAGTAACCAGGCCCAGGCACGGAGGAAG 1360
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                                                    574 LysAlaLeuGlnSerGlyProProGlnSerArgArgLys
                                                                                                                                                                                        Recombinant human lung tumour protein L523S.
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                                                                                                                ADA28517 standard; protein; 586
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98US-001231107.
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                                                             GlnGlyArg11eTyrGlyLys11eLysGluGluAsnPheValSerProLysGluGluVal
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LysAlaLeuGlnSerGlyProProGlnSerArgArgLys 586
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17-DEC-1999; 99US-00466396.
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10-JAN-2000; 2000US-00480894.
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which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCC
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                                       507 GlybysThrValAsnGluLeuGlnAsnLeuSerSerAlaGluValValValProArgAsp 526
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390 ProSerAlaMetThr----ProProTyrProGlnPheGluGlnSer---GluThrGlu 406
                                                                                             427 HisIleLysGlnLeuSerArgPheAlaGlyAlaSerIleLysIleAlaProAlaGluAla 446
CCCAGCAGCGTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAG 847
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Search completed: July 13, 2004, 12:08:40 Job time : 108 secs

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RESULT 1

US-09-261-855-2

US-09-261-855-2

Squence 2, Application US/09261855A

Patent No. 6255055

GENERAL INFORMATION:

APPLICANT: ROSS, Jeffrey

TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE

FILES REFERENCE: 960296-9313.1

CURRENT APPLICATION NUMBER: US/09/261,855A

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 577

TYPE: PRT

TYPE: PRT

TYPE: PRT

TYPE: PRT

US-09-261-855-2
Sequence 2, Appli
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Sequence 8, Appli
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Sequence 1731, A
Sequence 16789, A
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Best Local Similarity:
Query Match:
   Alignment Scores:
Pred. No.:
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-MODEL-frame+ n2p.model -DEV-xlp
-Q=/Cogn2 1/05FPTO spool p/USO9270437/runat 13072004 121922 9641/app query.fasta_1.1863
-DB=1Squed_Patents AA -QFWT-fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MARTIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 348, App
Sequence 348, App
Sequence 176, App
Sequence 176, App
Sequence 176, App
Sequence 176, App
Sequence 10, Appl
                                                                                                                      July 13, 2004, 12:07:12; Search time 22 Seconds (without alignments) 8016.105 Million cell updates/sec
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3110
1 agggacgctgccgcaccgcc.....atttccttcaggttttaaaa 1708
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11. /Ggn2_6/ptodatca/2/iaa/5A_COMB.pep:*
12. /Ggn2_6/ptodatca/2/iaa/5B_COMB.pep:*
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43. /Cgn2_6/ptodatca/2/iaa/6B_COMB.pep:*
55. /Cgn2_6/ptodatca/2/iaa/PcTUS_COMB.pep:*
6. /Cgn2_6/ptodatca/2/iaa/PcTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                     - protein search, using frame_plus_n2p model
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US-09-643-597-348
US-09-642-615A-348
US-09-66421B-348
US-09-643-597-176
US-09-480-884A-176
US-09-542-615A-176
US-09-60-421B-176
US-08-726-160-10
US-08-726-160-10
US-08-726-160-10
US-08-726-160-10
US-08-726-160-10
US-09-661-855-18
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext C
Ygapop 10.0, Ygapext C
Fgapop 6.0, Fgapext C
Delop 6.0, Delext C
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Maximum DB seq length: 200000000
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Perfect score:
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LysGlnLysProCysAspLeuProLeuArgLeuLeuValProThrGlnPheValGlyAla 209
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APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Misser, March A.W.
APPLICANT: Mondelson, Particia D.
APPLICANT: Mondelson, Particia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C11
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348
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Matches:
                                                                                                                                                           RESULT 2
US-09-643-597-348

Sequence 348, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
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74.17%
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Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
                                                                                                                                   573 GinAlaArgArgLys 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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| ProGluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMetHisLysGluAlaGln
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Matches:
Conservative:
Mismatches:
Indels: GENERAL INVOCATIONAL AND ADDITIONAL APPLICANT: Fan, Liqun APPLICANT: Fan, Liqun APPLICANT: Fan, Liqun APPLICANT: Barlos, Michael D. APPLICANT: Bargur, Chaitanya S. APPLICANT: Bargur, Chaitanya S. APPLICANT: Farger, Gary R. TITLE OF INVENTION: COMPCUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN FILE REFERENCE: 2010.1456268 CURRENT APPLICATION NUMBER: US/9542,615A CURRENT FILING DATE: 2000-04-14 NUMBER OF SEQ ID NOS: 350 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 348 LENGTH... 4.72e-146 1639.00 83.89% 74.17% 52.70% TYPE: PRT ORGANISM: Homo sapiens Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: 623

TYPE: PRT   CRGANISM: Homo sapiens   CRGANISM: Homo sapiens   CS-09-606-421B-348   CS-09-60	91	92 TACATCCCCGATGAGCAFAGCACAGGGACCTGAGAATGGGCGCCGAGGG	Oy 143 GGCTTTGGCTCTGGGGTCAGCCCGCCAGGCTCACCTGTGGCAGCGGGGGCCCCAGCC 202	Qy 203 AAGCAGCAAGAAGTGGACATCCCCTTCGGCTCCTGGTGCCCACCCA	0y         263 ATTATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATA 322           Db         210 IlelleGlyLySGluGlyAlaThrIleArgAsnlleThrLySGlnThrGlnSerLySile 229	Oy 323 GACGTGCATAGGAAGGAGAAGACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACC 382	Qy 383 CCTGAGGGCTGCTCCTCCGCTTGTAAGATCTTGGAGATTATGCATAAAGAGGCTAAG 442	Qy 443 GACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGG 502	Qy 503 CGTCTCATTGCAAGGACGGAACCTGAAGAAGGAAGGTAGAGCAAGATACCGAGACAAAA 562	Qy 563 ATCACCATCTCCTCGTTGCAAGACCTTACCCTTTACACCCTGAGAGGACCATCACTGTG 622	Qy 623 AAGGGGGCGATCGAGAATTGTTGCAGGGCGGAGGAATAATGAAGAAATTCGGGAG 682         :::        :::	Qy 683 GCCTATGAGAATGATGTGCGTGCCATGAGCTCTCACCTGATCCCTGGCCTGAAC 736 :::	Qy 737 CTGGCTGCTGTAGGCTTTTCCCAGCGCCAGCGCAGCGCGCGC	Qy 788 CCCAGCAGCGTTACTGGGGCTGCTATAAGCTCCTTTATGCAGCTCCCGAGCAGGAG 847	848 AIGGIGCAGGIGTITAICCCGCCCAGGCAGIGGGGGCGCCAICGCAAGAAGGGGGAGGGGAG	ProAlaLeuSerValGlyAlail
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APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Rance, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Briefer, A.W.
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Patent No. 6426072
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-643-597-176
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US-09-643-597-176
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Db 230 AspValHisArgLysGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThr 2  Qy 383 CCTGAGGGCTGCTCCTCCGCTTGTAAGATCTTGGAGATTATGCATAAAGAGGCTAAG 4	443 GACACCAAAACGGCTGAGGTTCCCCGAAGATCCCCGATAATAATTGTAGGGTTCCCCCCAAGAGGGTTGCTGAGGATCCCCAAGAGGGTTGTTGTAGGGTTTGTAGGGTTGTAGGGGTTGTT	Qy 503 CGTCTCATTGGCAAGGACGGAGCGGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAA 5	Qy 563 ATCACCATCTCGTTGCAAGACCTTACCAACACCTGAGGACCATCACTGTG 62.	Oy 623 AAGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGAATAATGAAGAAGGTTGGGAG 68:	Qy 683 GCCTATGAGAATGATGTGGCTGCCATGAGCTCTCACCTGATCCCTGGCCTGAAC 7 :::	Oy 737 CTGGCTGTAGGTCTTTTCCCAGCTTCATCCAGGCAGTCCCGCGGCCT 7	Qy 788 CCCAGCAGCAGTTACTGGGGCTGCTCATATAGCCTCCATTATGCAGGTCCCCGAGCAGGGG 847	Qy 848 AIGGIGCAGGIGITITAICCCCGCCCAGGCAGIGGCGCCCAICAICGCAGAAGAAGGGCCCA 907	Oy 908 CACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACA 967	Qy 968 CCTGACTCCAAAGTTCGTATGGTTATCATCACTCACCGCCAGAGGCCCAATTCAAGGCT 102:	1028 CAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTG		Qy 1148 GGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTGGTAGTACCAAGAGAC 120°	CAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGT	1268 CAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCAGG	Qy 1325 AAGGACAGAGTAACCAGGCCCAGGAAG 1360 	RESULT 7 US-09-542-615A-176 ; Sequence 176, Application US/09542615A
Db 487 LysLeuGluhlaHisIleArgValProSerPheAlaAlaGlyArgValIleGlyLysGly 506 Qy 1148 GGAAAAAGGGTGAAGTTGACGAATTTGACGCAGCTGAGGTGGTAGTACCAAGAGAC 1207	1208 CAGACCCCTATAGACAACAACAACAACATCATCGAACATTCTATGCCAGT 527	Oy 1268 CAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAG 1324	Qy 1325 AAGGGACAGAGTAACCAGGCCCAGGGAAGG 1360 	RESULT 6 US-09-480-884A-176 ; Sequence 176, Application US/09480884A ; Patent No. 6482597	GENERAL INFORMATION: ; APPLICANT: Wang, Tongtong ; APPLICANT: Fan, Liqun	APPLICANT: HOSKEN, MAINEY A. APPLICANT: Kalos, Michael D. APPLICANT: Fanger, Gary R. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY	; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER; FILE REFERENCE: 210121.455CG; CURRENT APPLICATION NUMBER: US/09/480,884A; CURRENT FILING DATE: 2001-08-27	NUMBER OF SEQ ID NOS: 330 SEQ ID NO 176 LENGTH: 579	/ TYPE: PKT / ORGANISM: Homo sapiens US-09-480-884A-176	Alignment Scores: 7.3e-146 Length: 579 Ford. No.: 1637.00 Matches: 336 Percent Similarity: 83.66\$ Conservative: 43 Percent Camilarity: 74.17\$ Minerthes: 68	52.64% Indels: 4 Gaps: 5 x US-09-480-884A-176 (1-579)	Qy         32 CGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCTGAAGGTCTCC         91           Dh         133 ArgGlaalafaniasanixsLanasanGlybhaGlufanGlubanPharbitanixsBala         152	92 TACATCCCCATGAGCAGATAGCACAGGGACCTGAGAATGGGGGCCCGAGGG 14	143 GGCTTTGGGGGTCAGCCCGCCGGGGGGGGGGGGGGGGGG	203 AAGCAGCAGCAAGCATGGACCTCCCCTTGGCTCCTGGTGCCCACCAGTATGTGGGTGCC	Qy 263 ATTATTGGCAAGGGGGCCACCATCGGAAAACAGACCCAGTCCAAGATA 322  Db 210 IleIleGlyLySGluGlyAlaThrIleArgAsnIleThrLySGlnThrGlnSerLySIle 229	Qy 323 GACGTGCATAGGAAGGAGAAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACC 382

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1088 AAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT 1147
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APPLICANT: Wang, Tongtong
APPLICANT: Ran, Ligun
APPLICANT: Ran, Chaitanya S.
APPLICANT: Rangur. Chaitanya S.
APPLICANT: Applicant: Hosken, Nancy
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPRENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
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                GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Range, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Banger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210221.4556
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 350
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Matches:
Conservative:
Mismatches:
Indels:
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83.66%
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CRGANISM: Homo sapiens
US-09-542-615A-176
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Best Local Similarity:
Query Match:
DB:
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                                                                                      447 ProAspAlaLysValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAla
                      CAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTG
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|IysAlaLeuGlnSerGlyProProGlnSerArgArgLys 579
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APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., ADM AVIGAM, MARK I.
TITLE OF INVENTION: NOYEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESCENCESCONDENCE: ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
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COMPUTER READABLE FORM:

MEDIUM TYPE: PLOBPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDDERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: 22-FEB-1993
CLASSIFICATION 375
PRIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-021-608D-10; Sequence 10, Application US/08021608D; Patent No. 5580760
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ATTORNEY/ACENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 643
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NEW YORK
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STATE: NE
COUNTRY:
ZIP: 1019
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Mismatches:
Indels:
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1637.00
83.66%
74.17%
52.64%
ORGANISM: Homo sapiens
                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
 , ORGANISM: Homo
US-09-606-421B-176
                                               Alignment Scores:
Pred. No.:
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|IeGlyArgAsnGlyGluMetileLySLySIleGlnAsnAspAlaGlyValArgIleGln 309
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483 yrAsnProAlaProTyrAsnProGlyProProGlyProAlaProHisGlyProProAlaP 503
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577 GlyGlnValAspTyrThrLysAlaTrpGluGluTyrTyrLysLysMetGlyGlnAlaVal 596
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ProProAspArgCysGlnHisAlaAlaGluIleIleThrAspLeuLeuArgSerValGln
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367 TrpAsnMetGlyProProGlyGlyLeuGln---GluPheAsnPheIleValProThrGly
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503 roTyrAlaProGlnGlyTrpGlyAsnAlaTyrProHisTrpGlnGlnGlnAlaProProA
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                                                            --AsnGluGlyIleAspValProIleProArgPheAlaValGlyIleVal
                                                                                                ATCGGCAAGAAGGGGCAGCACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAG
                                                                                                                                                              ATTGCACCACCGGAA----ACACCTGACTCCAAAGTTCGTATGGTTATCATCACGGA
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        ----SerArgIleGlyGly---
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                                                                                                                                                              Amino Acid 148 (Xaa) is Met or Ile
                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                    US-09-270-437D-5 (1-1708) x US-08-021-608D-10 (1-643)
                                                                                                                                                                                                                            Length:
Matches:
TYPE: Amino Acid
STRANDENESS: Single
TOPOLGGY: Unknown
MOLECULE TYPE: Peptide/Protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Human
CELL LINE: HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnLeuProProMetHis---
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248.50
37.80%
22.33%
7.99%
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OTHER INFORMATION:
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Best Local Similarity:
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US-08-021-608D-10
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1121 GCAGCTGGCCGGGTCATTGGCAAAGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACG 1180
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|ProProAspArgCysGlnHisAlaAlaGluIleIleThrAspLeuLeuArgSerValGln 346
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367 TrpAsnMetGlyProProGlyGlyLeuGln---GluPheAsnPheIleValProThrGly 385
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--GlnGlnGlnArg
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|------SerArgIleGlyGly
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88 GlnLeuProProMetHis---
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                                                                                                             Sequence 10, Application US/08726160

Patent No. 5734016

GENERAL INFORMATION:
APPLICANT: LEVEND. DAVID L., DUNCAN,
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ANDRESS:
ADDRESSEE: WORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2026-4063US1
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APPLICATION NUMBER: US/08/726,160
FILING DATE: 04-0CT-1996
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/021,608
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S: FELLER
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEMEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 643
                                                                                                                                                                                                                                                                                   SEE: MORGAN & FINNEGAN: 345 PARK AVENUE
NEW YORK
NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 20,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                  1687 AAATTTCCTTCAGGT 1701
                                         |||:::|||
597 ProAlaProThrGly 601
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248.50
37.80%
22.33%
7.99%
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
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EDNESS: Single
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MOLECULE TYPE: Pep
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Human
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                       CITY: NEW STATE: NI COUNTRY:
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PCT/US94/01782
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248.50
37.80%
22.33%
                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
STRANDBNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide/P
HYPOTHESTICAL: NO
ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
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Query Match:
DB:
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                                                                                                               1238 GTGAAAATCATCGGACAT-----TTCTATGCCAGTCAGATGGCTCAACGGAAG 1285
                                        1181 GCAGCTGAGGTGGTAGTACCAAGAGACCAGACCCCTGATGAGAACGACCAGGTC---ATC 1237
                                                                                                                                                                                          .286 AT-----CCGAGACATCCT---GGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAG 1335
                                                                                                                                                                                                                                                                     1336 TAACCAGGCCCAGGCACGGA----- 1373
                                                                                                                                                                                                                                                                                                                                                                                                                             CAACAACGGGCAGAAATCG 1413
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                                                                                                                                         426 PheThrileArgGlyThrProGlnGlnIleAspTyrAlaArgGlnLeulleGluGluLys 445
                                                                                                                                                                                                                                464
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                                                                      406 GlyAlaArgIleGluLeuGlnArgAsnProProProAsnAlaAspProAsnMetLysLeu 425
                                                                                                                                                                                                                                                                                               465 ---ProGlyPro--HisGlyProProGlyProProGlyProGlyThrProMetGlyProT 483
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569 Asp------GinglnAsnProAlaProAla 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549 GlnProProProAlaAlaProAlaGlyAlaProThrThrThrGlnThrAsnGlyGlnGly 568
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                                                                                                                                                                                                                  539 Tyr-----TyrAlaHisTyrTyrGlnGlnAla------TyrAlaHisTyrTyrGlnGlnGlnAla
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Sequence 10, Application PC/TUS9401782
Sequence 10, Application PC/TUS9401782
SEQUENCE 10: Application:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES
APPLICANT: AS REPRESSENTED BY THE SECRETARY, DEPARTMENT OF APPLICANT: HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                1374 ----CCTGTCCCTTNGAGTCCAGGA----
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPRFFECT 5.1
CURRENT APPLICATION DATA:
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ProAlaProThrGly 601
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155 CGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGCGGGGGCCCCCAGCCAAGCAGCAGCAGCAA 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 AAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 395 TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAA-----GAGGCTAAGGACACC 448
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157 GlnSerAlaLysArgLeuLeuAspGlnIleValGluLysGlyArgProAlaProGlyPhe 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 CCCGAT---GAGCAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGGGCCTTTGGCTCT 154
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CELL LINE:
CELL LINE:
ORGANELLE:
NAME/KEY:
LOCATION:
LOCATION:
OTHER INFORMATION: Amino Acid 148 (Xaa) is Met or Ile
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-270-437D-5 (1-1708) x PCT-US94-01782-10 (1-643)
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Indels:
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FILING DATE: 22-FEB-1994
CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FELLER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063PCT
TELECOMMUNICATION INFORMATICN:
TELECOMMUNICATION INFORMATICN:
TELESPAN: (212) 758-4800
TELESPAN: (212) 758-4819
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	Qy         1651 AAGAGGGTGGATCACCTCAGTGGGAAGAAATA 1686           :::       :::            :::      ::::             Db         577 GlyGlnValAspTyrThrLysAlaTrpGluGluTyrTyrLysLysMetGlyGlnAlaVal 596           Qy         1687 AAATTCCTTCAGGT 1701           Db         597 ProAlaProThrGly 601           RESULT 12         US-09-261-855-18           Sequence 18, Application US/09261855A         Patent No. 6255055           Patent No. 6255055         GENERAL INFORMATION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN           TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE           TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE           PILE REFERENCE: 960296.95131           CURRENT APPLICATION NUMBER: US/09/261,855A           VURRENT FILING BATE: 1999-03-03           NUMBER OF SEO ID NOS: 46	SOFTWARE: PatentIn Ver. 2.0   SOFTWARE: PatentIn Ver. 2.0   JENGTH: 49   TYPE: PRT   ORGANISM: Mus musculus   US-09-261-855-18   Alignment Scores: 5.86e-15   Dength: 49   Score: 245.00   Matches: 0   Percent Similarity: 100.00\$   Matches: 0   Percent Similarity: 100.00\$   Mismatches: 0   Ouery Match: 3   Gaps: 0   US-09-270-437D-5 (1-1708) x US-09-261-855-18 (1-49)	QY         476 ATCCTGGCCCATAATAACTTTGTAGGGGTCTCATTGGCAAGGAAGG
AAAACGGCTGACGACGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTA 49  HisHisGlyAspGlyProGlyAsnalaValGlnGluIleMetIleProAlaSerLysAla 19  GGGCGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAGATAGAAATACCGAGACA 55	268	AlaGlyAsnProGlyGlyProGlyGlyArgGlyArgGlyArgGlyArgGlyGaGaGaGaGaGaGaGaGaGaGaGaGaGaGaGaGaGaG	1238 GTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAG 1285 426 PheThrIleArgGlyThrProGlnGlnIleAspHyrAlaArgGlnLeuileGluGluLys 445 1286 ATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAG 1335 446 IleGlyGlyProValAsnProLeuGlyProProValProHisGlyProHisGlyVal 464 1336 TAACCAGGCCAGGCAGGAACAGA

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---ACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAG---GCCCAA 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1031 ------GGAAGAATCTATGGCAAACTCAAGGAGAAACTTCTTTGGTCCCAAG 1078
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297 MetileLysLysileGinAsnAspAlaGlyValArgileGinPheLysProAspAspGly 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 ThrGlyAspProTyrLysValGlnGlnAlaLysGluMetValLeuGluLeuIleArgAsp 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 LeuAspGlnIleValGluLysGlyArgProAlaProGlyPheHisHisGlyAspGlyPro 183
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222 IleGlnAsp------GlyProGlnAsnThrGlyAlaAspLysProLeuArgIle 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          623 AAGGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGAAATAATGAAGAAAGTTCGGGAG 682
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   ---GCCCCAGCCAAGCAGCAGCAAGTGGACATCCCCCTT----CGG 232
                                    85 PheGlyThrGlnLeuProProMetHisGlnGlnGlnSerArgSerValMetThrGluGlu 104
                                                                                            105 TyrLysValProAspGlyMetValGlyPheIleIleIlyArgGlyGlyGluGlnIleSer 124
                                                                                                                                               353 GCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGCTCCTCCGCTTGTAAGATG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                           518 GAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAATCACCATCTCCTCG 577
                                                                                                                                                                        ---GAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAAG
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                                                                                                                                                                                                                                                                                            413 ATCTTGGAGATTATGCATAAA----GAGGCTAAGGACACCAAAACGGCTGAC---
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---ProLeuGluAspGlyAspGlnProAspAlaLysLysValAlaProGlnAsnAspSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 AACCATGCCCTGAAGGTCTCCTACATCCCCGATGAGCAGATAGCACAG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-270-437D-5 (1-1708) x US-08-021-608D-2 (1-644)
                                                  APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                   CORPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
CURRENT APPLICATION DATA:
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
Sequence 2, Application US/08021608D
Patent No. 5580760
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: Single
TOPPLOGY: Unknown
MOLECULE TYPE: Peptide/Protein
HYPOTHETICAL: No
                                                                                                                                                                ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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36.46%
22.39%
7.88%
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
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                                                                          1199 CCAAGAGACCAGACCCCTGATGAGAACGACCAGGTC---ATCGTGAAAATCATCGGACAT 1255
                                                                                                                                                    -----TTCTATGCCAGTCAGATGGCTCAACGGAAGAT-----CCGAGACAT 1296
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| GlyLysGlyGlyGluThrIleLysSerIleSerGlnGlnSerGlyAlaArglleGluLeu 412
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                                                                                                                                                                                                                                                                                                                                          470 lyProProGlyProProGlyProGlyThrProMetGlyProTyrAsnProAlaProTyrA 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-726-160-2
Sequence 2, Application US/08726160
Patent No. 5/34016
GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
TITLE OF INVENTION:
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
TITLE OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 1015-4
ZIP: 1015-4
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPREFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,160
FILING DATE: 04-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 PheGlyThrGlnLeuProProMetHisGlnGlnGlnSerArgSerValMetThrGluGlu 104
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164 LeuAspGlnIleValGluLysGlyArgProAlaProGlyPheHisHisGlyAspGlyPro 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 AsnAspAlaPheLysAspAlaLeuGlnArgAlaArgGlnIleAlaAlaLysIleGlyGly 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION: Amino Acid 149 (Xaa) is Met or Ile
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148
93
202
33
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                  2026-4063US1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,608
FILING DATE: 22-FEB-1993
                                                                                                          REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644
                                                                                                                                                                                                                                                                               STRANDEDNESS: Single
TOPPLOGY: Unknown
MOLECULE TYPE: Peptide/Protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 TCACCTGTGGCAGCGGGG----
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245.00
36.46%
7.39%
                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 GAGAATGGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                 Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
CELL LINE: HL60
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Best Local Similarity:
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Db   258 GlnGlyGlyPheArgGluValArgAsnGluTyrGly	2908 2997 317	124 QY 1 175 Db 07 1 175 Db 08 1 193 Db 08 84 OY 1	104 Qy 1199 292 Db 413 124 Qy 1256 352 Db 433 143 Qy 1297 412 Db 453	eu 163  Oy 1354 GA
HAPLOTYPE: TISSUE TYPE: CELL TYPE: CELL TINE: HL60 ORGANELLE: NAME/KEY: LOCATION: LOCATION: COTHER INFORMATION: OTHER INFORMATION: Amino Acid 149 (Xaa) is Met or Ile	Alignment Scores:  Pred. No.:  Score:  Score:  Score:  Score:  245.00  Matches:  148  Percent Similarity:  26.46\$  Conservative:  93  Best Local Similarity:  7.88\$  Indels:  202  DB:  US-09-270-437D-5 (1-1708) x PCT-US94-01782-2 (1-644)	CCATGCCCTGAAGGTCTCCTACATCCCCGATGAG nAspAlabheLysAspAlaLeuGlnArgAlaArg GAATGGGCGCCGAGGGGGTTTGGC GAATGGGCGCCGAGGGGGTTTTGGC :::   palaGlyThrSerLeuAsnSerAsnAspTyrGly ACTGTGGCAGGGGG	PheGlyThrGlnLeuProProMetHisdlnGlnGlnSerArgSerValMetThrGluGlu CTCCTGGTGCCCACCAGTATGTGGGTGCCATTATTGGCAAGGAGGGGCCACCATCGG	ProGludrgSerCys***LeuThrGlyThrProGluSerValGlnSerAlaLysArgLeu ATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCAAAACGGCTGAC :::   :::   ::    :   LeuAspGlnIleValGluLysGlyArgProAlaProGlyPheHisHisGlyAspGlyProGAGGTTCCCCTGAAGATCTGGCCCATAATAACTTTGTAGGGCGTCCATTGGCAAG GlyAsnAlaValGlnGluCleMetIleProAlaSerLysAlaGlyLeu'allleGlyLys GAAGGACGAACCTGAAGATAGAGATACCGAGACAAAAATCACCATCTCCTCG  ::

TITIAAACGIGGAIIGTITAAAGAAGCICTCCAGGCCCCACCAAGAGGGIGGAICACAC 166		TCA	584 LysAlaTrpGluGluTyrTyrLysLysMetGlyGlnAlaValProAlaProThrGly 602	Search completed: July 13, 2004, 12:14:43 Job time : 47 secs
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APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Stang, Solam
APPLICANT: Tsang, Solam
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APPLICANT: Tsang, Solam
APPLICANT: Jager, Elke
APPLICANT: Odd, Lloyd J.
APPLICANT: Odd, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
TITLE OF INVENTION: Autigen, The Antigens Per Se, And Uses Thereof
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 5
Sequence 75, Appl
Sequence 11, Appl
Sequence 6251, Ap
Sequence 6420, Ap
Sequence 6339, Ap
Sequence 6775, Ap
Sequence 6775, Ap
Sequence 175, Ap
Sequence 183, Appl
Sequence 183, Appl
Sequence 183, Appl
Sequence 2813, Appl
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US-09-252-991A-6251

US-09-252-991A-6339

US-09-252-991A-6131

US-09-252-991A-6131

US-09-621-96-1331

US-09-621-976-15639

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99.7%; Score 1703; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1708; Conservative 0; Mismatches
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; Patent No. 6297364
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 7, Appli
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Sequence 4, Appli
                                                                              July 13, 2004, 17:54:49; Search time 134 Seconds (without alignments) 7073.553 Million cell updates/sec
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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*

6. /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-899-651-5
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US-09-613-85-11
US-09-613-897-347
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US-09-613-897-347
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US-09-825-497A-40
US-09-825-497A-39
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330 ATAGGAAGGAGAGGGGGGGGGGGGAAAAAGCCATCAGTGGCACTCCACCCCTGAGG 389 568 ATAGGAAGGAGAACGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGG 627 508 GCTGGTCCTCCGCTTGTAGATGATTATGCATAAAGAGCACTCCACCCCTGAGG 627 590 GCTGGTCCTCCGCTTGTAAGATGATTATGCATAAAGAGGCTAAGGACACCA 449 [	CCATCGAGATTGTTGCAGGCCGAGCAGAATTATGAAGAAAGTTCGGGGGCCTATG CCATCGAGATTGTTGCAGGCCGAGCAGAATTATGAAGAAAGTTCGGGGGGCCTATG CCATCGAGATTGTTGCAGGCCGAGCAGAATTATGAAGAAAAGTTCGGGGGGCCTATG CCATCGAGATTGTTGCAGGCCGAGCAGAATTATGAAGAAAATTATGAAGAATCGGGGGCCTATG AGAATTGTTGCAGGCCGAGCAGAAATTATGAAGAAATTATGAGCCCTGAACCTGGCCTGACCTGCTGTTGAAGAAAAGAAGACTCCCGGCCTGACCTGGCCTGACCTGCTGTTGAGGCTCCTGAGCTCCTGACCTGGCCTGACCTGACCTGCTGTTGAGGCTCCTGAGCTCCTGAGCTCCTGAGCTCTCTGAGGCTCCTGAGCTCCTGACCTGACCTGACCTGACCTGACCTGAGCTCTCTTGAGGCTCCCGAGCAGCAGCTCCTGAGCTGCTCTGAGGCTCCTGAGGCTCCTGAGCTCCTGAGCTCCTGAGCTCCTGAGCTCCTGAGCTCCTGAGCAGCTTATTATCCCGGCTTATTATCCCGGCAGCAGCAAAAGAGGCAACCTAAACAACACTTTATCCCGGCTTATTATCCCCGGCTTATTATCCCCGAGCAGCAGAAAAAGAGGCAACCTAAACAACACTCCCCGGCTATTATCCCCGGCTTATTATCCCCGAGCAGCAGAAAAAAAA	

Db   2024 AGAACAATGTTCCAGTGAGAATCCTGATCTCTGCCCCCAATTGAGCCAGCTGGCCA 2081   1562 CAACACTGTNTGCCCTCGGGGTGTCAGAATTNTAGCGGAAGGACTTTTAAACGTGGA 1621   1   1   1   1   1   1   1   1   1	### SESULT 6    SEGURATE   197-347	Db   522   TGGGCAGGGCTCCTCAAGGGTCTCCAGGATCCTATCCAGGAACATG   SB1
	AGAATGATGATGGCCATGAGCTCTCACCTGATCCCTGGCCTGAACCTGGTG  AGAATGATGATGTGCCATGAGCTTGCAGTCCCTCCTCTGGCCTTAACTG  CTGTAGGTCTTTTCCCAGCTTCATCCAGCGCTGCTCCTCCTCCTCCTCCTCGGCTTAACTG  CTGTAGGTCTTTTCCCAGCTTCATCCAGCGCTGCTCCTCCTCCTCCCTC	1785 1344 1845 1403 1905 1942 1965

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1002 GACATGTGCCAAAGCTGAGGAGGATCATGAAGAAAATCAGGGAGTCTTATGAAAATGA 1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522 TGGGCAGAGGGGCTCCTCAAGGCAGGGTCTCCAGGATCCGTATCCAAGCAGAAACCATG 581
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                                                         FOR THERAPY CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                            34.1%; Score 582.2; DB 4; larity 66.2%; Pred. No. 2.8e-156; Conservative 0; Mismatches 433;
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAL
FILE REPREMENCE: 210121.45568
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 347
                                                                                                                                                                                                                                                                                                             TYPE: DNA
, ORGANISM: Homo sapiens
US-09-542-615A-347
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RESULT 7
US-09-542-615A-347
Sequence 347, Application US/09542615A
Perent No. 6518256
GENERAL INFORMATION:
APPLICANT: Mang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.

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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur. (Chaitanya S.
APPLICANT: Bangur. (Chaitanya S.
APPLICANT: Panger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AMD DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
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CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FASUSEQ for Windows Version 3.0
SEQ ID NO 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 347, Application US/09606421B Patent No. 6531315 GENERAL INFORMATION:
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Best Local Similarity
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	1312   TSTGGCTGCCATGAGCTCTCACCTGATCCTGGCCTGAACCTGGCTGTAGG 750   1312   TATTGCTTCATGAATCTCAAGCACTTTAATTCCTGGAATTAATCTGAACGCCTTGGG 1371   1312   TATTGCTTCATGAATCTCAAGCACTTTTAATTCCTGGAATTAATCTGAACGCCTTGGG 1371   1312   TATTGCTTCATCAATTCAAGCACTCCCGCCACCTCAGGCGCTTTAACCCATGAACTCCACCCCCTCAGGCGCTTTAACCCACCACCACCACCACCACCACCACTTAACCCATGAACTCAAGCACTCAAGCACTCAAGCACTTAACCACGACACACAC	MESULT 10  15-09-899-651-4  15 Sequence 4, Application US/09899651  15 Patent No. 6576756  16 Patent No. 6576756  17 APPLICANT: Chen, Yao-Tseng  18 APPLICANT: Teang  19 APPLICANT: Teang  19 APPLICANT: Teang  10 APPLICANT: Accrete, Elisabeth  10 APPLICANT: Absorber, Elke  11 APPLICANT: Muth, Alexander  11 APPLICANT: Muth, Alexander  11 APPLICANT: Assorberd  11 TILE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer  11 TILE OF INVENTION: Associated  12 TILE OF INVENTION: Associated  13 CURRENT APPLICATION NUMBER: US/09/899, 651  13 CURRENT PILING DATE: 2001-07-06  15 PRIOR APPLICATION NUMBER: US/09/061, 709
	4, Application US/09061709B 4, Application US/09061709B 118POMATION: 1	
Cy 1231 GGTCATCGTGAAAAT	PRESULT 9 US-09-061-709-4 Sequence 4, Application US/09061709B Petent No. 6297364 GENERAL INFORMATION: APPLICANT: Chen, Yac-Tseng APPLICANT: Stockert, Blisabeth APPLICANT: Order, Ala APPLICANT: Order, Ale APPLICANT: Order, Ale APPLICANT: Order, Blisabeth APPLICANT: Order, Ale APPLICANT: Order, Blisabeth APPLICANT: Orde	277 892 337 952 397 1012 457 1072 517

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       TGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTATGGT
                                                                            TATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACT
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APPLICANT: Honderson, Robert A.
APPLICANT: Mordellly Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US(99/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SRQ ID NO 175
LENGTH: 4181
                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 175, Application US/09643597; Patent No. 6426072; GENERAL INFORMATION:
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Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aljun
Skeiky, Yasir A.W.
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LOCATION: (3347)
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                                                                                                                                                          Query Match 34.0%; Score 580.6; DB 4; Best Local Similarity 66.1%; Pred. No. 1.2e-155; Matches 857; Conservative 0; Mismatches 434;
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
LENGTH: 4159
TYPE: DNA
ORGANISM: HOMO SADIENS
                                                                                                              ; FEAIURE:
US-09-899-651-4
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Pactent No. 6482537

CENERAL INFORMATION:
APPLICANT: Wang, Torgtong
APPLICANT: Fan, Ligun
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ranger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF SERRENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 175
LENGTH: 4181
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Pred. No. 1.2e-155;
0; Mismatches 434;
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US-09-643-597-175
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Best Local Similarity 66.1%;
Matches 857; Conservative
n=A, T, C
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LOCATION: (4080)
OTHER INFORMATION: n:
NAME/KEY: unsure
LOCATION: (4088)
OTHER INFORMATION: n
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OTHER INFORMATION: D. MAME/KEY: UNSURE LOCATION: (3974)
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NAME/KEY: unsure
LOCATION: (3940)
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LOCATION: (4062)
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                                                                                                                                                                    1672 TAAAGAAGAAAACTTTGTTAGTCCTAAAGAAGAGGTGAAACTTGAAGCTCATATCAGAGT
                                                                                                                                                                                                                1111 GCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCA
                                                            TATCATCACTGGACCGCCAGAGGCCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACT
                                                                                                 1612 GATTATCACTGGACCACCAGAGGCTCAGTTCAAGGCTCAGGGAAGAATTTATGGAAAAAT
                                                                                                                                       1051 CAAGGAGGAGACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGT
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APPLICANT: Fan, Ligun
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Mancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1912 GGAAATTCTGACTCAGGTAAAGCAGCACCAACAG 1948
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, Patent No. 6510826
, Patent INFORMATION:
, APPLICANT: Wang, Tongtong
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OTHER INFORMATION: n=A,T,C or
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ORGANISM: Homo sapiens
PRATURE:
NAME/KEY:
LOCATION: (3347)
OTHER INFORMATION: n=A,T
NAME/KEY: unsure
LOCATION: (3502)
OTHER INFORMATION: n=A,T
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LOCATION: (3506)
OTHER INFORMATION: DAME/KEY: unsure
LOCATION: (3520)
OTHER INFORMATION: n
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LOCATION: (3549)
OTHER INFORMATION: 1
NAME/KEY: unsure
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LOCATION: (3538)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 CICCGCTIGTAAGAIGAICTIGGAGAITATGCAIAAAGAGGCTAAGGACACCAAAACGGC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAA 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAATTGTTGCAGGCCGAGCAGGAAATAATGAAGAAAGTTCGGGAGGCCTATGAGAATGA 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGAGATGGTGCAGGTGTTTATCCCCCGC 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      871 CCAGGCAGTGGGCGCCATCATCGGCAAAGAGGGCAGCACATCAAACAGCTCTCCCGGTT 930
                                                                                                                                                                                                                                                                                                               CCCCGATGAGCACATAGCACAGGGACCTGAGAATGGGCGCCCGAGGGGGCTTTGGCTCTCG 156
                                                                                                                                                                                                                                                                                                                                                                                          GGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGCGGGGGCCCCAGCCAAGCAGCAGCAAGT 216
                                                                                                                                                                                                                                                                                                                                                                                                                   217 GGACATCCCCCTTCGGCTCCTGGTGCCCAGTATGTGGGTGCCATTATTGGCAAGGA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGATTTGCCTCTGCCCTGCTGCTTCCCACCCAATTTGTTGGAGCCATCATAGGAAAAGA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGCCACCATCCGCAACATCACAAAACAGACCCAAGTCCAAGATAGACGTGCATAGGAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGCTC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        517 GGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATCACCATCTCCTC 576
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                                                                                                                                                                                                                                                                         AGCACTAGACAAACTGAATTGGATTTGAGTTAGAGAATTTCACCTTGAAAGTAGCCTATAT 711
                                                                                                                                                                                                                                                                                                                                                    712 CCCTGATGAAATGGCCGCCCAGCAAAACCCCTTGCAGCAGCCCGAGGTCGCCGGGGGGCT 771
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                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                  9
                                                                                                                                                          Length 4181;
                                                                                                                                                                                                Indels
                                                                                                                                                            Query Match 34.0%; Score 580.6; DB 4; Best Local Similarity 66.1%; Pred. No. 1.2e-155; Matches 857; Conservative 0; Mismatches 434;
    ; TYPE: DNA; GOGANISM: Homo sapiens; FEATURE:
; NAME/KEY: misc_feature; COCATION: (1)...(4181)
; OTHER INFORMATION: n=A,T,C or GUS-09-480-884A-175
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AGTGGTTGTCAAAATAACTGGTCACTTCTATGCTTGCCAGGTTGCCCAGAAAAATTCA 1911
                                                                                   1612 GATTATCACTGGACCCACCAGAGGCTCAGTTCAAGGCTCAGGGAAGAATTTATGGAAAAAT
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Lidgun
APPLICANT: Fan, Lidgun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hanger, Mancy
APPLICANT: Hanger, Nancy
APPLICANT: Hanger, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W,
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTIAND NOS: 358
SOFTIAND NO 175
FURNATION: AND 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 1.2e-155;
0; Mismatches 434;
                                                                                                                                                                                                                                                                                                                                                           | LOCATION: (4080)
| OTHER INFORMATION: n=A,T,C or G
| NAME/KEY: unsure
| LOCATION: (4088)
| OTHER INFORMATION: n=A,T,C or G
| NAME/KEY: unsure
| LOCATION: (4115)
| OTHER INFORMATION: n=A,T,C or G
| US-09-542-615A-175
                                                       LOCATION: (3968)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (3974)
OTHER INFORMATION: n=A,T,C or G
LOCATION: (4036)
OTHER INFORMATION: n=A,T,C or G
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                        LOCATION: (4056)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (4062)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
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Best Local Similarity 66.1%;
Matches 857; Conservative
                       n=A, T, C
LOCATION: (3940)
OTHER INFORMATION:
NAME/KEY: unsure
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FEATURE: NAME/KEY: unsure LOCATION: (3347)	Qy 97 CCCGATGAGCAGATAGCACAGGACC	
OTHER INFORMATION: n=A,T,C or G FEATURE:	Db 712 ĆĆĆTGATGAAATĠGCCĠĆCĊĀĠCAAA	CCCTGATGAAATGGCCGCCCAGGAAAACCCCTTGCAGCAGCCCCGAGGTCGCCGGGGGCT 771
NAME/KEY: unsure LOCATION: (3502)	2y 157 GGGTCAGCCCGCCAGGGCTCACCTGT	
õ	Db 772 TGGGCAGAGGGGCTCCTCAAGGCAGG	TGGGCAGAGGGCTCCTCAAGGCAGGGGTCTCCAGGATCCGTATCCAAGCAGAAACCATG 831
AME/I	QY 217 GGACATCCCCCTTCGGCTCCTGGTGCC	GGACATCCCCTTCGGCTCCTGGTGCCCACTATGTGGGGTGCCATTATTGGCAAGGA 276
OTHER INFORMATION: n=A,T,C or G	Db 832 reArrieccrcreciccrecrearic	ccacccaatrigingaagccarcaragaaaaaa 891
Y: unsure N: (3520)	Qy 277 GGGGGCCACCATCGGAACATCACAAA	GGGGGCCACCACCACACACACAAACAGACCCAGTCCAGATAGACGTGCATAGGAA 336
7, 7	337	
LOCATION: (3538)  LOCATION: (3538)  DIFFR INFORMATION: n=A,T,C or G	952	AGAAAATGCGGGGGCTGCTGAGAAGTCGATTACTATCCTCTCTACTGAAGGCACCTC 1011
FALURE: NAME/KEY: UCCATION: (3549) OTHER INFORMATION: n=A,T,C or G	Qy 397 CTCCGCTIGTAAGATGATCTTGGAGAT 	CTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCAAAACGGC 456 
FEATURE: NAME/KEY: unsure LOCATION: (3646) OTHER INFORMATION: n=A,T,C or G	Qy 457 TGACGAGGTTCCCCTGAAGATCCTGGC 	TGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGCGTCTCATTGGCAA 
FEATURE: NAME/KEY: unsure LOCATION: (3940) OTHER INFORMATION: n=A.T.C or G	517	
	577	
OTHER INFORMATION: n=A,T,C or G FEATURE:	1192	
NAME/KEY: unsure LOCATION: (3974) THER INFORMATION: n=A,T,C or G	Qy 637 GAATTGTTGCAGGGCCGAGCAGGAAAI 	GAATTGTTGCAGGGCCGAGCAGGAAATAATGAAGAAGTTCGGGAGGCCTATGAGAATGA 696 
FEATURE: NAME/KEY: unsure LOCATION: (4036) OTHER INFORMATION: n=A,T,C or G	Qy 697 TGTGGCTGCCATGAGCTCTCP	TGTGGCTGCCATGAGCTCTCACCTGATCCCTGGCCTGAACCTGGCTGCTGTAGG 750
FEATURE: NAME/KEY: unsure LOCATION: (4056) OTHER INFORMATION: n=A,T,C or G	Qy 751 TCTTTTCCCAGCTTCATCCAGGGCAGT	TCTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGGCTGC 810
n=A.		TCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATCGTGCAGGTGTTTATCCCGG 870
	871	
LOCATION: (4080) COTHER INFORMATION: n=A,T,C or G	Db 1492 TCTATCAGTCGGTGCCATCATCGGCAA	TCTATCAGTCGGTGCCATCATCGGCAAGGCCAGCAGCACATCAAGCAGCTTTCTCGCTT 1551
	931	TGCCAGCGCCTCCATCAAGATTGCACCCGAAACACCTGACTCCAAAGTTCGTATGGT 990
OTHER INFORMATION: n=A,T,C or G FEATURE:	1552	
NAME/KEY: unsure LOCATION: (4115) OTHER INFORMATION: n=A,T,C or G	Qy 991 TATCATCACTGACGCCAGAGGCCCA 	TATCATCACTGGACGCCGAGGCCCCATTCAAGGCTCAGGAAGAATCTATGGCAACT 1050
Query Match 34.0%; Score 580.6; DB 4; Length 4181; Seet Local Similarity 66.1%; Pred. No. 1.2e-155;	Qy 1051 CAAGAGAGAAACTICTIIGGTCCCAA	CAAGGAGAGAACTICTITGGICCCAAGGAGGAAGTGAAGCTGGAGGCCCACATACGTGI 1110 
Macches 85/7 Conservative 07 Mismatches 454; Indels 9, Gaps 37 AGCCATCATGAAGCTGAATGGCACCAGTTGGAGAACCATGCCTGAAGGTCTCCTACAT	Qy 1111 GCCAGCATCAGCAGCTGGCCGGGTCAT	GCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAAGGGGGAAAAAGGGTGAACGAGTTGCA 1170 
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Fatent No. 6297364

GENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng

APPLICANT: Tsang, Solam

APPLICANT: Muth, Alexander

APPLICANT: Did, UN Solated Nucleic Acid Molecules Encoding Cancer Associated

TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof

FILE REPERENCE: LUD 5538

CURRENT APPLICATION NUMBER: US/09/061,709B

CURRENT FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 8
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JOURNAL Patent: US 6297364-A S 02-OCT-2001; FEATURES  Location/Qualifiers  1.1708  /mol_type="unassigned DNA"  ORIGIN  Query Match  Query Match  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1708; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Matches 1708; Conservative 0; Mismatches 0; Indels 0; Oppose 0;  AGGGACGCACCCCACTTACCCCGGGAGCCATGAAGGCCA 60  Db 1 AGGACCTCCGCACCCCCCAGTTACCCCGGGGGAGCCATCATGAAGCTGAATGGCCA 60	61 61 121 121 121 181	241 GCCCACCCAGTATGTGGGGTGCCATTATTGGCAAGGAGGGGCCACCATCCGCAACATCAC  241 GCCCACCCAGTATGTGGGTGCCATTATTGGCAAGGAGGGGCCACCATCCGCAACATCAC  301 AAAACAGACCCAGTCCAAGATAGACGTGCATTAGGCAAGAAGGAGGGGGCCACCACCACCAGGAAGAAA  301 AAAACAGACCCAGTCCAAGATAGACGTGCATAGGAAGGAA	Qy         361         AGCCATCAGTGGACTCCACCCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTGGA         420           Db         361         AGCCATCAGTGTCCACCCCTGAGGGCTCCTCCGCTTGTAAGATGATCTTGGA         420           Qy         421         GATTATGCATAAAGAGCTAAGGACACCAAAACGGCTGACGAGGTTCCCCTGAAGATCCT         480           Db         421         GATTATGCATAAAGAGCTAAGGACACCAAAACGGCTGACGGAGGTTCCCCTGAAGATCCT         480           Qy         481         GGCCCATAATAACTTTGTAGGGCTCTCATTGGCAAGGAAGG	541 AGAGAAGATCCAAAAATCACATCTCCTCGTGCAAGACCTTACAAAATAACATAACATTAACAAAATAACATTAACAAAATAAAAATAACATTAACAAAAATAAAAATAACATTAACAAAAAA	AGAATGAIGTGGCGATGAGCTCTCACCT	0y 781 GCGCCTCCCAGCAGCGTTACTGGGGCTGCTTTATGCAGGTCCCCA 840 Db 781 GCCGCCTCCCAGCAGCGTTACTGGGGCTGCTCTTATGCAGGTCCCA 840 Db 781 GCCGCCTCCCAGCAGCGTTACTGGGGCTGCTCCTTATGCAGGTCCCA 840 Qy 841 GCAGGAGATGGTGCAGGTGTTATCCCGCCCAGCAGTGGGCCCATCATGGCAGAA 900 Db 841 GCAGGAGATGGTGCAGGTGTTTATCCCGCCCAGGCAGTGGCCCATCATGGCAGAA 900 Qy 901 GGGGCAGCATTATATCCCCGCCCAGGCAGTGGCCATCATGGCAGAAA 900 Qy 901 GGGGCAGCATTAATCCCCGCCCAGGCCCATCAGGCAAGAA 900

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1 (bases 1 to 1708)
Chen, V.T., Gure, A., Tsang, S., Stockert, E., Jager, E., Knuth, A. and Old, L.J.
Isolated nucleic acid molecules encoding cancer-associated antigens, these antigens and method of using the same patent: UP 2002512049-A 3 23-APR-2002;
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PC 112N15/09, A61K35/12, A61K39/00, A61K39/39, A61P35/00, C07K16/32, PC 12N1/15,
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DEFINITION Sequence 7 from patent US 6297364.  ACCESSION AR171866 AR171866.1 GI:17910816 KEYMORDS SOURCE ORGANISM Unclassified.  TITLE Isolated nucleic acid molecule encoding cancer associated antigen, the antigen tiself, and uses thereof JOURNAL Patent: US 6297364.A 7 02-OCT-2001, FEATURES SOURCE AUTHOR Seas 1 to 1946) AUTHOR Chan'S A Tang, S., Stockert, E., Jager, E., Alexander, K.  TITLE Isolated nucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof JOURNAL Patent: US 6297364.A 7 02-OCT-2001, FEATURES SOURCE //Organism="unknown" //ORIGIN ORIGIN	Query Match         97.7%;         Score 1669.2;         DB 6;         Length 1946;           Best Local Similarity         99.8%;         Pred. No. 0;         3         Indels 0;         Gaps 0;           QY         30 CCGGGGAGCCATCATGAAGGTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCT 89         B         B         B           Db         268 CCAGGCAAGCCATCATGAATGGCCACCAGTTGGAGAACCTTGAGAGGTCT 327         CTACATCCCCGATGAAGCCACAGGAACCAGAAACCATGCTTG 149           QY         90 CCTACATCCCCAGTGAAGAGAAACCAGGAACCAGAGAACCAGAGAATGCTTG 149	328 CCTACATCCCCGATGAGCAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGGGGCTTTG  150 GCTCTCGGGGTCAGCCCGCCAGGGCTCACCTGTGGCGGGGGCCCCAGCCAAGCAGC  11	DD	QY         390         GCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCA 449           bb         628         GCTGCTCCTCGTGTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCA 687           QY         450         AAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCA 509           Db         688         AAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCA 509	OY         510 TTGGCAAGGAAGGAACCTGAAGAAGTAGAAGAAGTACCGAGACAAAAATCACCA 569           Db         748 TTGGCAAGGAAGGAACCTGAAGAAGTAGAAGATACCGAGACAAAATCACCA 807           Qy         570 TCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAAGAGACCATCACTGTGAAGAGG 629           Db         808 TCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAAGAGACCATCACTGTAAAGAGG 867	Oy 630 CCATCGAGAATTGTTGCAGGGCCGACAGAAATAATGAAGAAAGTTCGGGAGGCCTATG 689

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BD209926 15-JUL-2003 1946 bp DNA linear PAT 17-JUL-2003 Isolated nucleic acid molecules encoding cancer-associated antigens, these antigens and method of using the same.
BD20926.1 GI:33019696 JP SO05212049-A/5.
Homo sapiens (human)
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Chen, Y.T., Gure, A., Tsang, S., Stockert, E., Jager, E., Knuth, A. and old, L.J.
Isolated nucleic acid molecules encoding cancer-associated
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LUDMIG INSTITUTE FOR CANCER RESEARCH
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PD 33-APR-2002
PF 16-MAR-1999 US 09/061709
PF 17-APR-1999 US 09/061709
PT ALEXANDER KNUTH, LLOYD J OLD
PC C12N15/09, A61K35/12, A61K39/00, A61K39/39, A61P35/00, C07K16/32, PC C12N1/15,
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1. 1946
1. 1946
Aorganism="Homo sapiens"
| //organism="Homo sapiens"
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| //ordanism="lost" | //organism="lost" | //
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n=not determined(1622,1702,1771,1809,1833)
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Location/Qualifiers
Location/Qualifiers
1. 1946
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Matches 1676; C
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PDEHAMMKAIETFSGKVELGGKRIETEHSVPKKGRSRKIQIRNIPPQULKWEVLDSLLA
QGGTVENCEGVWTESFTAVVVVYSNREGJTRQAIMKLNGHQLENHALKVSYIPDEQIA
QGPENGRRGGFGSRGOPRQESPVAGARPAKQQQVDIPLKLLVPTQVVGAIIGKEGATI
RNITKQTQSKIDVHRKENAGAAEKAISVHSTPEGGSSACKVILLEIMHKEAKDTKYADE
VPKKILAHNNFVGRLIGKERNLKKVERODTERTTTISSLQDTTANREAKDTKYADE
NCCRAEQEIMKKVNERNIQAERNLKKVERODTERTTTISSLQDTTANREAKDTKYADE
NCCRAEQEIMKKVNERNIQAEMNLKGODTERTTTISSLQDTTANRESSTTTVKGAIE
NCCRAEQEIMKKVNERNIQAEMSLGSHILFGLINLAAVGIFPASSSAVPPPPSSK
AAPYSSFMQAPEQEMVQVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSK
                 26-JAN-1999
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TVNELQNLTAAEVVVPRDQTPDENDQVIVKI I GHFYASQMAQRKIRDILAQVKQQHQK
GQSNQAQARRK"
                                                                                                                                                                                                                                                             2 (bases 1 to 2130)
Nielsen,J., Christiansen,J., Lykke-Andersen,J., Johnsen,A.H.,
Nielsen,J., Christiansen,J., Lykke-Andersen,J., Johnsen,A.H.,
Diwerr,U.M. and Nielsen,F.C.
Direct Submission
Submitted (30-DEC-1998) Institute of Molecular Biology, University
of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark
L. 2130
/organism="Homo sapiens"
/db xref="mRNA"
/db xref="mRNA"
/db xref="mRNA"
/li - 2130
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              PRI 26-JAN-199
mRNA, complete
                                                                                                           Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 2130)
Mielsen, J., Christiansen, J., Lykke-Andersen, J., Johnsen, A.H.,
Wewer, U.M. and Nielsen, F.C.
A family of insulin-like growth factor II mRNA-binding proteins
Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               .0. .1743
|gene="IMP-1"
|note="binds multiple sites in IGF-II mRNA 5'UTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2130;
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                AF117106 2130 bp mRNA linear
Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
product="IGF-II mRNA-binding protein 1"
protein id="AAD09826.1"
/db_xrefe="GI:4191608"
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Pred. No. 0;
0; Mismatches
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AF117106.1 GI:4191607
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[0. .1743
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                                                                                               Homo sapiens (human)
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             LOCUS
DEFINITION
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                                                                                      ATAGGAAGGAGCACCCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCTGAGG
                                                                                                                   ATAGGAAGGAAGGAGAGCTGAAAAAAGCCATCAGTGTGCACTCCACCCCTGAGG
                                                                                                                                                                                              GCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAAGGACACCA
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NCCRAEQEIMKKVREAYENDVAAMSLQSHLTPGLNLAAVGLFPASSSAVPPPPSSVTG
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I (bases 1 to 2381)

I coannidis,P., Trangas,T., Dimitriadis,E., Samiotaki,M., Panouteakopoulos,G., Kyriazoglou,I., Voutzoulias,S.,S.,

Tsiapalis,C.M., Kittas,C., Agnanis,N. and Pandis,N. and Pandis,N. and Pandis,N. and Pandis,N. and Pandis,N. and Pandis,N. betopic expression of a KH-domain containing protein, highly homologous to both human IMP-1 and mouse CRD-BP, in benign and malignant mesenchymal tumors

I Unpublished to 23.07

I Direct Submission

I Cannidis,P., Trangas,T., Dimitriadis,E. and Samiotaki,M.

Direct Submission

I Cannidis,P., Trangas,T., Dimitriadis,E. and Samiotaki,M.

Direct Submission

I Cation/Qualifiers

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I Cation
         CCCAGGCACGGAGGAAGTGACCAGCCCCTCCCTGTCCTTCGAGTCCAGGACAACGG 1783
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                                                                                GCAGAAATGAGAGTGTGTCTCCCCGGCAGGCCTGAGAATGAGTGGGAATCCGGGACAC
                                                                                                                                                                         CTGGGCCGGCTGTAGATCAGGTTTGCCCCACTTGATTGAGAAAGATGTTCCAGTGAGGAA
                                                                                                                                                                                                                                        CCCTGATCINICAGCCCCAAACACCCCACCAATIGGCCCCAACACTGINIGCCCCTCGGGG
                                                                                                                                                                                                                                                                        CCCTGATCTCTCAGCCCCAAACACCCACCAATTGGCCCAACACTGTCTGCCCCCTCGGGG
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                                                       GCAGAAATCGAGAGTGTGCTCTCCCCGGCAGGCCTGAGAATGAGTGGGAATCCGGGACAC
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mRNA, complete
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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Homo sapiens (human)
JP 2002017375-A/3242
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                    CC C12P21/02,C12Q1/68//C12P21/08,G06P17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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 HELIX RESEARCH INSTITUTE
OS Home sapiens (Numan)
PN J2-2020101375-A/3242
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAL, KOJI HAYASHI, SHIZUI SHII,
PI SHII,
PI SHII,
PI SHII,
PI TETSUJI OTSUKI, HISASHI KOGA
PI TETSUJI OTSUKI, HISASHI KOGA
CIZNIS/09, CO7XL4/47, CO7XL6/18, CIZNI/15, CIZNI/19, CIZNI/21, CIZNS/
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Primer for synthesizing full-length cDNA and use thereof.
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G1:23222756
JP 2002017375-A/3242.
Homo sapiens (human)
Homo sapiens (human)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
GTATGGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCAGCATCAGAAGGGACAGAGTAACCAGG
                                                                                                                         1044 GCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACA
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Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 3242 22-JAN-2002;
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REFERENCE 2 (bases 1 to 2780)  AUTHORS  Jurect Submission  JOURNAL  Submitted (125-MR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  (E-mail:genomics@hrico.jp, Tel:81-438-52-3986)  NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA Huli insert sequencing: Research Association for Biotechnology; CDNA ilbrary constructing: Research Association for Biotechnology; CDNA ilbrary construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).  Augustic Research Institute (supported cation/Qualifiers  Location/Qualifiers  Augustic Research Institute (supported cation/Lype="max" Augustic Research Institute Augustic Research Institute Augustic Research Institute Augustic Research Institute August	Query Match         81.3%;         Score 1389;         DB 9;         Length 2780;           Best Local Similarity         99.2%;         Pred. No. 0;         0.0	QY         359 AAAGCCATCAGTGGCACTCCACCCTGAGGGCTGCTCCGCTTGTAAGATGATCTTG 418           Db         61 AAAGCCATCAGTGCACTCCACCCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTG 120           QY         419 GAGATTATGCATAAAGAGCTAAAGAACACCAAAACGGCTGACGACGAGGTTCCCCTGAAGATC 478           Db         121 GAGATTATGCATAAAGAGCTAAAGGACACCAAAACGGCTGACGAGGTTCCCCTGAAGATC 180	Qy         479 CTGGCCCATAATAACTTTGTAGGGGGTCTCATTGGCAAGGAAGG	Oy         599         PACCTGAGAGGACCATCACTGTGAAGGGGGCAATTGTTGCAGGGCCGAGCAG         658           Db         301         AACCCTGAGAGGACCATCACTGTGAAGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAG         360           Qy         659         GAAATAATGAAGAAGACCTATGAGAATGATGGTGGCTGCATGAGCCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG
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                                          Score 1165; DB 6;
Pred. No. 1.8e-282;
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/mol_type="unassigned DNA"
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/translation="MNKLYIGNLNESVTPWKQRSKTQIRNI PPOLKMEVDSLLA
PDEHWAMAALETSESGKVELDENERPERGESKTQIRNI PPOLKMEVDSLLA
QVGTVENCRQVNTESETAVNVTVSNREGPRAQOPUDIPLALLVPTQYVGAIIGKEGATI
RNITKGTQSKIDVHRKENAGAABEALSVHSPEGGSSCKTMILENHRKZAKDTKTADE
VPLKILAHNNFVGRLIGKSGRNLKKVEQDTSTKITISSLQDLTLYNPFRTITVKGAIE
NCCRAEQEINKKVRRAYENDYAAMSLOGSHLIFGLNLAAVGLFPASSSSAVPPPPSSYTG
AAPVSSFMQAPEDENVQVFTPAQAVGAIIGKKGQHIKQLSRRAASIKIAPPETPDSK
VRMVVITGPPEAQFKAQGRIYGKLKENFFGPKESVKLETHINVPASAAGRVIGKGGK
TVNBLQNLTAABVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDLLAQVKQCHQK
GQSNLAQARRK"
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Doyle, G.A., Betz, N.A., Leeds, P.F., Fleisig, A.J., Prokipcak, R.D.
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Leeds,P., Kren,B.T., Boylan,J.M., Betz,N.A., Steer,C.J.,
Gruppuso,P.A. and Ross,J.
Developmental regulation of CRD-BP, an RNA-binding protein that
stabilizes c-myc mRNA in vitro
Oncogene 14 (11), 1279-1286 (1997)
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ribosome translocation
Mol. Cell. Biol. 14 (3), 2119-2128 (1994)
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Ross, J., Prokipcak, R.D., Leeds, P., Doyle, G.A.R., Betz, N.A.
Fleisig, A.J.
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Submitted (25-APR-1998) McArdle Laboratory, University (
- Madison, 1400 University Ave., Madison, WI 53706, USA
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Prokipcak, R.D., Herrick, D.J. and Ross, J.

Purification and properties of a protein that C-terminal coding region of human c-myc mRNA Biol. Chem. 269 (12), 9261-9269 (1994)

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (2023)
Bernstein, P.L., Herrick, D.J., Prokipcak, R.D. and Ross, J.
Control of c-myc mRNA half-life in vitro by a protein capable of Genes Dev. 6 (4), 642-654 (1992)
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Herrick,D.J. and Ross,J.
The half-life of c-myc mRNA in growing and serum-stimulated cells:
                                              1485 GAATGGTCGTCATCACTGGACCCCCAGAGGCTCAGTTCAAGGCTCAGGGAAGAATTTATG
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S GGTCTCGGGGCCAGCCCGGGCAAGGGTCGCCCGTGGCAGGAGGGCCTCCAGCCAAGCAGC  AGCAAGTGGACATCCCCTTCGGCTCCTGGTGCCACTATGTTGTTGTTTTGTTTTTTTT	OY 390 GCTGCTCCTCGCCTTGTAGATGATTTATGCATAAAGAGATAACAACA 449	Oy 510 TTGGCAAGGAAGGACCTGAAGAAGGTACAGCAAGATACCGAGACAAAAATCACCA 569	CTATG      TTACG	690 AGAAIGAIGTGGCCTGCCAIGAGCTCTCACCTGATCCCTGGCCTGACCTGGCTG	OY 744 CTGTAGGTCTTTTCCCAGCTTCATCCAGCGCAGTCCGCCGCCTCCCAGCAGCGTTACTG 803	OY 804 GGCTGCTCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGAGATGGTGCAGGTGTTTA 863	Oy 864 TCCCGGCCAGCAGTGGGCGCCATCATCGGCAAGAAGGGCAGCACATCAAACAGCTCT 923	Oy 924 CCCGGTTTGCCAGCCTCCATCAAGATTGCACCACCGAAACACCTGACTCCAAGTTC 983	OY 984 GTATGGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATG 1043	Oy 1044 GCAAACTCAAGGAGAGAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACA 1103 	Oy 1104 TACGTGTGCCAGCATCAGCAGCTGGGTCATTGGCAAAGGTGGAAAACGGTGAACG 1163  Db 1605 TACGGGTTCCGGCTTCAGCAGCCGGCGTCATCGGCAAAGGGGGGAAAACGGTGAATG 1664	OY 1164 AGTTGCAGAATTTGACGCCAGCTGAGGTGGTAGTACCAAGAGACCAGACCCTGATGAGA 1223	OY 1224 ACGACCAGGICATCGTGAAAATCATCGGACATTTTATGCCAGTCAGATGGCTCAACGGA 1283 Db 1725 ACGACCAAGTCATTGTTAAGATCATCGGACATTTTTATGCCAGCCA

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                                                                                                                                      CCTACATCCCCGATGAGCAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGGGGCTTTG 149
                                                                                                                                                                    CCTACATACCTGATGAGGGAGATAACGCAAGGTCCTGAGAATGGGCGTCGTGGAGGCTTG 808
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                                                                                                                                                                                                                                                                                                               CCAGGCAAGCTATCATGAAGCTAAATGGCCATCAACTGGAGAACCATGCCCTGAAGGTCT
                                                                                                                                                                                                                GCTCTCGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGCGGGGGCCCCAAGCCAGC
                                                                                                                                                                                                                                                GGTCTCGGGGCCAGCCCCGGCAAGGGTCGCCCGTGGCAGCAGGGGCTCCAGCCAAGCAGC
                                                                                                                                                                                                                                                                                       CCATTGAGAACTGTTGCAGGGCCGAGCAGGAGATCATGAAGAAAGTTCGAGAGGCTTACG
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                                                               CCCGGGGAGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACACA
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                                                                                                                                                                                                                                                                                                                                                                                                      929 GCAAGGAGGGTGCCACCATCCGAAACATCACAAACAGAGGCGAGTCCAAAATAGACGTGC
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         Pred. No. 1.3e-281;
0; Mismatches 264;
         larity 82.6%;
Conservative
         Best Local Similarity
Matches 1410; Conserv
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRMVVITGPPEAĞFKAĞGRIYGKLKEBNFFGPKĒBVKLETHIRVPASAAGRVIGKGK
TVNELQNLTAAEVVVPRDQTPDENDQVIVKIIGHFYASQMAQRKIRDILAQVKQQHQK
                                                                                                                                                                                                                                        Sequencing Center
Center code: BCM-HGSC
Center code: BCM-HGSC
Center code: http://www.bgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu.kov. Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
 Submitted (30-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
                                                                                                                                      e
                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Kenneth R. Boheler (National Institute
Aging, USA)
                                                                                                                                                                cDNA Library Preparation: Yulan Piao and Minoru Ko (National Institute on Aging, NIH: http://lgsun.grc.nia.nih.gov/cDNA/) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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/clone="MGC:60613 IMAGE:30008106"
/tissue_type="ES Cell; undifferentiated, mouse, R1
Embryonic stem cells"
/clone lib="NIA Mouse Undifferentiated ES Cell CDNA
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"note="KH", Region: K homology RNA-binding domain"
'db_xref="CDD:smart00322"
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/note="RRM; Region: RNA recognition motif"
/dbxref="CDD:smart00360"
877. .1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 1.2444
| gene="19f12pl" | MP-1, Neilsen, CRD-BP"
| mote="synonyms: IMP-1, Neilsen, CRD-BP"
| CAD_xref="LocusID:140486"
| CAD_xref="MGI:1890357"
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                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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'db_xref="CDD:smart00322"
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/lab_host="DH10B"
/note="Vector: pSPORT1"
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/ Godon start=1
/ produCt="b-actin zipcode binding protein 1"
/ produCt="b-actin zipcode binding protein 1"
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OYGTVENCEQVNTESETJAVNAVYSNREGYRQAIPTRILVPTQYVGAIIGKEGATI
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VRMVVITGPPEAQFKAQGRIYGKLKENFFGPKEEVKLETHHRVPAARASIKTAPPSK
TVNBLQNITAARAVVTGVPEAQFKAQGRIYGKLKENFFGPKEEVKLETHHRVPAARASIKTAPPSK
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TVNBLQNITAARAVVTROPPEAQFKAQGNIYGKLENFFGPKEEVKLETHHRVPAARAKRINDILAQVKQQHQK
GQSNQAQARRK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1112.4; DB 10; Length
Pred. No. 3.2e-269;
0; Mismatches 178; Indels
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|strain="Sprague-Dawley"
                                                                                               'db_xref="taxon:10116'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.1%; Scor.
86.2%; Prec
                                                                                                                223. .1956
/note="rZBP1"
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Best Local Similarity
Matches 1285; Conserv
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                                                                                                                                                                                                                                                                                                                    2008
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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(bases 1 to 2105)

Eom,T., Antar,L.N., Singer,R.H. and Bassell,G.J.
Localization of a beta-actin messenger ribonucleoprotein complex with zipcode-binding protein modulates the density of dendritic filopodia and filopodial synapses
J. Neurosci. 23 (32), 10433-10444 (2003)
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Eom.T., Singer, R.H. and Bassell, G.J.
Direct Submission
Submitted (27-AUG-2002) Neuroscience, Albert Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
                                                                  1769 TACGGGTTCCGGCTTCAGCAGCCGGCCGTGTCATCGGCAAAGGCGCAAAAACGGTGAATG
                                                                                                                                                                                                                    CCCAGGCACGGAGGAGTGA - CCAGCCCCTCTCCCTTTNGAGTCCAGGACAACG
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  GCAAACTAAAAGAAGAATTTCTTTGGTCCCAAGGAGGAAGTAAAGCTAGAGACCCACA
                                                                                                                    AGTTGCAGAATTTGACGGCAGCTGAGGTAGTACCAAGAGACCAGACCCCTGATGAGA
                                                                                                                                             AGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAGTAACCAGG
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                                         TACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAAGGTGGAAAAACGGTGAACG
                                                                                                                                                                                                 ACGACCAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGA
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/ GOGOD STATE = 1
/ POCOUTE = "SEQUENTIAL STANDARD PROCESSION OF STATE = 1
/ POCOUTE = "Zipcode-binding protein"
/ protein id="MARBA2295.1"
/ db xref="GI: 257091"
/ translation="MNKLYIGNLNESVTPADLEKVFNDHKISFSGQFLVKSGYAFVDC PDEQNAMKAIEFSESGXVELHGKQLETHSYPKKQRSKYIGIRINIPPOLGNAMVLDGLLA QYGTVENGGQVNTDSETAVNVYTYNREGTRQAIMKLNGHQLENHVLKVSYIPPOGSV QGPENGRRGGFGARGAPROSSPVTAGAPVKQQPVDIPLRLLYPPOYVGYIIGKEGATI RNITKGTOSKIDVHKENGGAEKAISIHSTPEGGSAACKMILEIMQKEAKDTKTADE VPLKILAHNNFVGRLIGKEGRNLKKVEQDTFKITISSLQDLTLYNPERTITVKGSIE NCCKARQEINKKVREAYENDYAMSLQSHLIFGLINLANGGLEPASSNAVPPPPSSSVSG AAPYSSERWEPEGETVVYVFIPAQAVGAIIGKKGQHIKQLSRFASASIKIAPPETPDSKV
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vnelonltaaevvvprdotpdeneqvi vki i ghfyasqmaqrki rdi laqvkqqhqkg
osqolqarr"
                                                                                                            2 (bases 1 to 2021)
Oleynikov,Y.S., Ross,A.F. and Singer,R.H.
Direct Submission
Submitted (24-SEP-1997) Cell Biology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10461, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="binds a zipcode element in beta-actin
3'UTR and is involved in its localization"
note="beta-actin mRNA zipcode-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nuclear localization signal; NLS'
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.larity 81.3%; Pred. No. 2.1e-219;
Conservative 0; Mismatches 242;
       Mol. Cell. Biol. 17 (4), 2158-2165 (1997)
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/gene="ZBP1"
/note="encodes KH-domain #4"
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                                                                                                                                                                                                                                                                                                                                                                 /organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="texon:0031"
/cell_type="fibroblast"
/dev_stage="embryo"
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/gene="ZBP1"
/note="encodes R
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129. .1859
/gene="ZBP1"
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/gene="ZBP1"
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/gene="ZBP1"
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/gene="ZBP1"
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/gene="ZBP1'
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/gene="ZBP1"
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                                              1277 AGAATGACGTGGCCATGAGCTTGCAGTCTCACCTCATCCCTGGTCTCAACCTGGCTG
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Gallus gallus
Gallus gallus
Eukaryota, Marcaa, Chordata, Craniata, Vertebrata, Euteleosto
Archosauria, Aves; Neognathae, Galliformes; Phasianidae,
Phasianinae, Gallus.
1 (bases 1 to 2021)
Ross, A.F., Oleynikov,Y., Kislauskis,E.H., Taneja,K.L. and
Singer,R.H.
Characterization of a beta-actin mRNA zipcode-binding protein
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CTACATCCCGATGAGCAGATAGCACAGGACCTGAGAATGGGGGCCGAGGGGGCTTTG 149	GCTCTCGGGGTCAGCCCGGCCAGGGCTCACCTGTGGCAGGGGGGCCCCAGCCAAGCAGC 209	AGCAAATGGACATCCCCCTTCGGCTCCTGGTGCCCACCCA	GCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGCCCAGTCCAAGATAGACGTGC 329	ATAGGAAGGAACGCAGGTGCAGCTGAAAAACCCATCCACTCCACCCTGAGG 389	GCTGCTCCTCCGCTTGTBAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACA 449 	AAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGGGTCTCA 509	TIGGCAAGGAAGGAGGGAACCIGAAGAAGGIAGAGCAAGAIACCGAGACAAAAATCACCA 569 	CTCCTCGTTGCAAGACCTTACCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGG 629	GAGAATTGTTGCAGGCCGAGCAGGAAATAATGAAGAAAGTTCGGGAGCCTATG 689 	TIGGCTGCCATGAGCTCTCACCTGATCCTGGCTGACCTGGCTG 743	CTGTAGGTCTTTTCCCAGCTTCATCCAGGCAGTCCCGCGCCCTCCCAGCAGCGGTTACTG 803	GGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGAGATGGTGCAGGTGTTTA 863	TCCCGCCCAGGCAGTGGGCGATCATCGGCAAGAAGGGGCAGCACATCAAACAGCTCT 923 	CCCGGTTTGCCAGGCCTCCATCAAGATTGCACCACCGGAAACACCTGACTCCAAAGTTC 983 	GTATGGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATG 1043 	GCAAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGACACCCACA 1103 	TACGIGIGCCAGCATCACAGCAGCTGGCCGGGTCATTGGCAAAGGGGGAAAACGGTGAACG 1163
90 CCTACATCCCCGATGAGCA( 	150 GCTCTCGGGGTCAGCCCCGGGGTCAGCCCCCGGGGTCACCCCCCGGGGTCCCCCCGGGGTGCCCCCCGGGGTGCCCCCC	210 AGCAAGTGGACATCCCCCTT 	270 GCAAGGAGGGGGCCACCAT 	330 ATAGGAAGGAGAACGCAGG 	390 GCTGCTCCTCCGCTTGTAA 	450 AAACGGCTGACGAGGTTCC	510 TTGGCAAGGAAGCACGGAA 	570 TCTCCTCGTTGCAAGACCTT	630 CCATCGAGAATTGTTGCAG	690 AGAATGATGTGGCTGCCAU	744 CTGTAGGTCTTTTCCCAGC	804 GGGCTGCTCCCTATAGCTC 1303 GGCTGCTCCATACAGCTC	864 TCCCGGCCCAGGCAGTGGG 	924 CCCGGTTTGCCAGCGCCTC	984 GTATGGTTATCATCACTGG 	1044 GCAAACTCAAGGAGGAGAAA 	1104 TACGTGTGCCAGCATCAGC

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(without alignments)
10510.849 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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1708
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		,			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
н	1703	99.7	1708	6	_	Sequence 5. Appli
0	1669.2	97.7	1946	6	US-09-899-651-7	Sequence 7. Appli
ო ს	1283.6	75.2	1738	16	US-10-062-674-2082	Sequence 2082. Ap
4,	1165	68.2	2224	6	US-09-873-637-1	Sequence 1, Appli
S	1085.4	63.5	1182	σ	US-09-764-864-327	Sequence 327, App
9	1069.8	62.6	1129	σ	US-09-764~864-745	
7	582.2	34.1	1740	6	US-09-735-705-347	347
80	582.2	34.1	1740	9	US-09-850-716A-347	347
Q	582.2	34.1	1740	σ	US-09-897-778-347	347
10	582.2	34.1	1740	13	US-10-007-700-347	
11	582.2	34.1	1740	15	US-10-117-982-347	Seguence 347, App
12	582.2	34.1	1740	15	US-10-117-982-478	Sequence 478, App
13	582.2	34.1	1740	16	US-10-313-986-347	Seguence 347. App
14	582.2	34.1	1740	16	US-10-313-986-478	Sequence 478. App

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Gaps

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DB 9; Length 1708; 0; Indels

Query Match
99.7%; Score 1703; Di
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1708; Conservative 0; Mismatches

TYPE: DNA ORGANISM: Homo sapiens

, reaton. US-09-899-651-5

FEATURE:

LENGIH: 1708

SEQ ID NO 5

9

61 CCAGTIGGAGAACCATGCCCTGAAGGTCTCCTACATCCCCGATGAGCAGATAGCACAGGG 120

1 AGGGACGCTGCCGCACCCCCCAGTTTACCCCGGGGAGCCATCATGAAGCTGAATGGCCA 60 1 AGGACGCTGCCGCACCCCCAGTTTACCCCGGGGAGCCATCATGAAGCTGAATGGCCA

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	RESULT 4  Sequence 1, Application US/09873637  Sequence 1. Application US/09873637  Patent No. US/02002061543A1  GENERAL INFORMATION: THE C-MC CODING REGION DETERMINANT-BINDING PROTEIN  TITLE OF INTENTION: THE C-MC CODING REGION DETERMINANT-BINDING PROTEIN  TITLE OF INTENTION: THE C-MC CODING REGION DETERMINANT-BINDING PROTEIN  TITLE OF INTENTION: THE C-MC CODING REGION DETERMINANT-BINDING PROTEIN  TITLE OF INTENTION: THE C-MC CODING REGION DETERMINANT-BINDING PROTEIN  TITLE OF INTENTION: THE C-MC CODING REGION DETERMINANT-BINDING PROTEIN  CURRENT PILING DATE: 2001-06-04  SOFTWARE: Patentin Ver. 2.0  SEQ ID NOS: 46  SEQ ID NOS: 46  SEQ ID NOS: 46  SEQ ID NOS: 46  SEG ID
150 GCTCTCGGGGTCAGCCCGGCAGGGCTCACCTGTGGCAGCGGGGGCCCAGCCAG	684 CCINTGAGAATGATGTGGCTGCATGAGCTCTCACCTGATCCCTGGACCTGAACC 1015  1075 CCTATGAGAATGATGTGGCTGCCATGAGCCTGCACTGATCCCTGGCTGG

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Best Local Similarity 98.7%;
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US-09-764-864-745
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NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 745
LENGTH: 1129
TYPE: DNA
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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     CTGCCCCTCGGGGTGTCAGAATTCTAGCGCAAGGCACTTTTAAACGTGGATTGTTTAAA
                                                                                                 GAAGCTCTCCAGGCCCCACCAAGAGGGTGGATCACACCTCAGTGGGAAGAAAAATT
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GENERAL INFORMATION:
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hender, Nancy
APPLICANT: Wang, Aljun
APPLICANT: Wesky, Yasir A.W.
APPLICANT: Menderson, Robert A.
APPLICANT: Menderson, Robert A.
APPLICANT: Menderson, Robert A.
APPLICANT: Morbill, Particia D.
APPLICANT: Morbill, Particia D.
APPLICANT: Morbill, Particia D.
APPLICANT: Panger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 347, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
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US-09-735-705-347
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822 AGAAGAGATCCCCTTGAAGATTTTAGCTCATAATAACTTTGTTGGACGTCTTATTGGTAA
                                                                                          GGAAGGACGGAACCTGAAGAAGTAGACAAGATACCGAGACAAAAATCACCATCTCCTC
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Sequence 347, Application Us/09850716A
Sequence 347, Application Us/09850716A
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455015
CURRENT APPLICATION NUMBER: US/09/850,716A

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                                                                                 TGCCAGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGCAGAAGTTCGTATGGT
                                                                                                                                                                                   1302 TGCTGGAGCTTCAATTAAGATTGCTCCAGCGGAAGCACCAGATGCTAAAGTGAGGATGGT
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APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Panger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT FILLING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
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66.2%; Pred. No. 6.9e-171;
ive 0; Mismatches 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 347, Application US/09897778; Patent No. US20020147143A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Tongtong
APPLICANT: Wange, Tongtong
APPLICANT: Warnerakis, Margarita
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 858; Conserv
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US-09-897-778-347
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                                                                                                                                                                               Length 1740;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                          Score 582.2; DB 9;
Pred. No. 6.9e-171;
0; Mismatches 433;
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFIWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 347
                                                                                                                                                                            34.1%;
                                                                                                                                                                      Query Match
Best Local Similarity 66.2<sup>3</sup>
Matches 858; Conservative
                                                                                             TYPE: DNA
CRGANISM: Homo sapiens
US-09-850-716A-347
                                                                               LENGTH: 1740
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GROWSHAL INCOMPANION:
GROWSHAL INCOMPANION:
APPLICANT: Wang, Aijun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Nebert A.
APPLICANT: Fanger, Nebert A.
APPLICANT: Fanger, Neil
APPLICANT: Fanger, Neil
APPLICANT: Fanger, Neil
APPLICANT: Fanger, Neil
APPLICANT: Fanger, Sary R.
APPLICANT: Fanger, Sary R.
APPLICANT: Panger, Towns S.
APPLICANT: Panger, Veshihiro
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Neil
APPLICANT: Carter, Sochihiro
APPLICANT: Carter, Poy, Teresa M.
APPLICANT: Carter, Poy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND PLAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455617
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT PLING BATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SCOFTWARE: FastSEQ for Windows Version 4.0
TURNOR 1100 347
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larity 66.2%; Pred. No. 6.9e-171
Conservative 0; Mismatches 433
                                                                                                             US-10-007-700-347
; Sequence 347, Application US/10007700
; Publication No. US20030064947A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C18
CURRENT APPLICATION NUMBER: US/10/117,982
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 484
SOFTWARE: RESURENCE FOR Windows Version 4.0
LENGTH: 1740
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                                                                                                                                                                                                                                               Score 582.2; DB 15;
Pred. No. 6.9e-171;
0; Mismatches 433;
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Best Local Similarity 66.2'
Matches 858; Conservative
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ORGANISM: Homo sapiens
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Sequence 347, Application US/10117982
Publication No. US20030138438A1
GENERAL INFORMATION
APPLICANT: Foy, Teresa M.
APPLICANT: Foy, Teresa M.
APPLICANT: Poyer, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Wedvick, Thomas S.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Kalos, Michael D.
APPLICANT: Spies, Gregory A.
APPLICANT: Fanderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Fanderson, Robert A.
APPLICANT: Fan, Liqun

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Pred. No. 6.9e-171;
0; Mismatches 433; Indels 6;
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| Publication No. US2003013843841
| GRDERAL INPORMATION:
| APPLICANT: Fory, Teres M. |
| APPLICANT: Fanger, Gary R. |
| APPLICANT: Garter, Darrick |
| APPLICANT: Watanabe, Yoshihiro |
| APPLICANT: Matanabe, Yoshihiro |
| APPLICANT: Mericle |
| APPLICANT: Mericle |
| APPLICANT: Spies, Gregory A. |
| APPLICANT: Wang, Tongtong |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER |
| TITLE REFERENCE: 21012.455C18 |
| CURRENT APPLICATION NUMBER: US/10/117,982 |
| WUMBER OF SEQ ID NOS: 484 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENGTH. 1740
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Best Local Similarity 66.2%;
Matches 858; Conservative
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US-10-117-982-478
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| Sequence 478, Application US/10313986
| Publication No. US20030236209A1
| GENERAL INFORMATION:
| APPLICANT: FORMATION:
| APPLICANT: MCNabb, Andria
| APPLICANT: Watanabe, Yoshihiro
| APPLICANT: Warg, Tongtong
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: COMPOSITIONS AND METHODS
| FILE REFERENCE: 210121.455C19
| CURRENT APPLICATION NUMBER: US/10/313,986
| CURRENT FILING DATE: 2002-12-04
| NUMBER OF SEQ ID NOS: 560
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 1740
| TYPE: DNA
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                                             GGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCG
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| Publication No. US20030236209A1
| GRUERAL INFORMATION:
| APPLICANT: FORMATION:
| APPLICANT: MCNabb, Andria
| APPLICANT: MCNabb, AND INCOMENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
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Pred. No. 6.9e-171;
0; Mismatches 433;
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cal Similarity 66.2%;
858; Conservative
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US-10-313-986-347
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Best Local S:
Matches 858
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GGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAGATCCG 1290
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   GATTATCACTGGACCACCAGAGGCTCAGTTCAAGGCTCAGGGAAGAATTTATGGAAAAAT 1421
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                                                                                                       GCCAGCATCAGCAGCTGGCCATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCA
                                                                                                                                                                            GAATTTGACGGCAGCTGAGGTGGTAGTACCAAGAGACCAGACCCCTGATGAGAACGACCA
                                      CAAGGAGAGAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGT
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Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Pengar, Noil
APPLICANT: Pengar, Noil
APPLICANT: Pengar, Noil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT APPLICATION NUMBER: US/09/897,778
NUMBER OF SEQ ID NOS: 467
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Pred. No. 6.9e-171;
0; Mismatches 433;
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66.2%;
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Best Local Similarity 66.2
Matches 858; Conservative
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ORGANISM: Homo sapiens
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                                                     DB 16; Length 1740;
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                                                  Score 582.2; DB 16;
Pred. No. 6.9e-171;
0; Mismatches 433;
                                                  34.18;
                                              Query Match
Best Local Similarity 66.2°
Matches 858; Conservative
; ORGANISM: Homo sapiens
US-10-313-986-478
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Search completed: July 13, 2004, 23:41:03 Job time : 798 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

July 13, 2004, 14:50:27 ; Search time 699 Seconds (without alignments) 10380.433 Million cell updates/sec Run on:

US-09-270-437D-5 Title: Perfect score:

Sequence:

Scoring table:

Searched:

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6747726 Total number of hits satisfying chosen parameters: 3373863 segs, 2124099041 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqn2001bs:\* geneseqn2002s:\* geneseqn2003as:\* N\_Geneseq\_29Jan04:\* 1: qeneseqn1980s:\* geneseqn2000s:\* geneseqn2001as:\* geneseqn2003bs:\* geneseqn2003cs:\* geneseqn1990s:\* geneseqn1980s:\* geneseqn2004s: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Aaz36151 DNA encod	An	Aak94782 Human ful	- w	48 Human	Abx73489 Human nov	Human		Human		Aac66035 Human lun	Abl49254 Human lun	Human		Human	Abq92483 Human lun	Human	Ada28540 Recombina	Ada28537 Recombina	Abl49283 Human lun	Abq92469 Human lun	Ada28518 Recombina	Ada28437 Human lun
ΩI	AAZ36151	AAZ36153	AAK94782	AAZ10617	AAS26148	ABX73489	AAS26566	ABX73907	AAK91969	AAK93655	AAC66035	ABL49254	ABQ92440	ABL49299	ABL49297	ABQ92483	ABQ92485	ADA28540	ADA28537	ABL49283	ABQ92469	ADA28518	ADA28437
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## ALIGNMENTS

RESULT 1

DNA encoding cancer associated antigen KOC-2. AAZ36151 standard; DNA; 1708 BP. (first entry) Homo sapiens. 11-FEB-2000 AAZ36151; AAZ3615. 

Cancer associated antigen; KOC-2; cancer; vaccine; CT7; ss.

WO9954738-A1.

28-OCT-1999.

99WO-US005766. 16-MAR-1999; 98US-00061709. 17-APR-1998; (LUDW-) LUDWIG INST CANCER RES.

Jager E, Stockert E, Gure A, Tsang S, WPI; 2000-013284/01. Chen Y,

old LJ;

Knuth A,

Nuclectides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers.

Claim 55; Page 40; 44pp; English.

The present sequence represents a cancer associated antigen gene designated KOC-2. The specification also describes a cancer associated antigen designated CC-2. The CT7 polymucleotide was isolated from SK-MEL-37 melanoma cells. The polymeptide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAX43877. The CT7 polymeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polymucleotides and polymeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony

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                                           CAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGAGAACTTCTTTGGTCCCAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of DNA encoding cancer associated antigen KOC-2.
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                                                           Length 1708;
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Nucleotides representing cancer-associated genes, used to develo products for the diagnosis, monitoring and treatment of cancers. Claim 55; Page 42; 44pp; English LUDWIG INST CANCER RES WPI; 2000-013284/01 Gure A, Chen Y, 

The present sequence represents an alternative form of a cancer associated antigen gene designated KOC-2. The specification also describes a denoter associated antigen designated CT7. The CT7 polynucleotide was isolated from SX-WEL-37 melanoma cells. The CT7 polynucleotide was some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats fich in serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAY43877. The CT7 polypeptide can be processed to peptides which provoke lysis by evtolytic T cells. The polynucleotides and polypeptides can be used for treating a Cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony stimulating factor (GM-CSF)

Sequence 1946 BP; 502 A; 528 C; 553 G; 358 T; 0 U; 5 Other;

ö 327 149 387 209 269 329 449 569 629 447 507 567 389 627 687 509 747 867 807 83 CCTACATCCCCGATGAGGAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGGGGGCTTTG ccadecaadccarcardaadcreaardeccaccacracardeccardeccreaaggrer CCTACATCCCCGATGAGCAGATAGCACAGGACCTGAGAATGGGCGCCGAGGGGCTTTTG GCAAGGAGGGCCACCATCCGCAACATCAAAAAAAAGACCCAGTCCAAGATAGACGTGC ATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGCACTCCACCCCTGAGG ATAGGAAGAAACGCAGGTGCAGATGAAAAACCCATCACTGTGTGTCCACCCCCTGAGG TTGGCAAGGAAGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATCACCA TCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGG CCCGGGGGGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCT GCTCTCGGGGTCAGCCCCGGCCAGGGCTCACCTGTGGCAGCGGGGGCCCCCAGCCAAGCAGC GCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCA AAACGGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCA AAACGGCTGACGAGGTTCCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCA 748 TTGGCAAGGAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAATCACCA TCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGG Gaps Score 1669.2; DB 3; Length 1946; Pred. No. 0; 0; Mismatches 3; Indels 0; 3; Indels Query Match
Best Local Similarity 99.8%;
Matches 1676; Conservative 448 330 568 390 688 30 268 328 150 388 210 270 628 450 510 570 90 ઠ d  $\delta$ 쉱 à qq ઠે d ò g δ 임 ò g ò 셤 ઠે 셤 δ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length cDnes were obtained by construction of full length enrished cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length muman cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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                                                                                                                                                             full length cDNA; cDNA synthesis; oligo-capping; ss.
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K, Kojima S,
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                                    AAK94782 standard; cDNA; 2780
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                                                                                                           <u> ATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGG</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing presence or absence of a tumor in a human by examining c-myc coding region determinant-binding protein.
                                                                                                                                                                                                          region determinant binding protein.
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Best Local Similarity 82.7%;
Matches 1409; Conservative
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      CCCAGGCACGGAGGAAGTGA-CCAGCCCCTCCCTGTCCCTTNGAGTCCAGGACAACAACG 1402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac artest; cerebrovascular disorder; cerebral ischaemia; angiogenesis, nervous system disorder; Alzheimer's disease; infection; ocular disorder; conneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                      AGAACAATGTTCCAGTGAGGAATCCTGATCTCTCGCCCCCAA--TTGAGCCAGCTGGCCA
                                                                                                                                    -------ATCGAGAGTGTGCTCTCCCCGGCAGGCCTGAG
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15-MAR-2000; 2000US-0199076P.

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and New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives. Claim 1; SEQ ID NO 327; 980pp; English

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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a plathological condition. Antibodies to the proteins can also be used in alloyating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune

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diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. arreadisc arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Arbieimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to respente tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, mirerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed 1074 1254 1314 1134 ACCACCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGC 1014 CATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGGCAGCTGAGGTGGT 1194 GCAGCATCAGAAGGGACAGAGTAACCAGGCCCAAGGCACGGAGGAAGTGACCAGCCCCTCC 1374 CIGICCCTINGAGICCAGGACAACAAGGGGCAGAAAICGAGAGIGIGCICTCCCCGGCAG 1434 617 677 797 437 497 9 AATAATGAAGAAGTTCGGGAGGCCTATGAGAATGATGTGGCTGCCATGAGC-----TC 714 137 774 reaccidarecereacerdaecreciderariamentreceaecricareages 197 834 257 894 TCCCGAGCAGAGATGGTGCAGGTGTTTATCCCGCCCAGGCAGTGGGCGCCATCATCGG 317 CAAGAAGGGGAGCACATCAAACAGCTCTCCCGGTTTTGCCAGCGCCTCCATCAAGATTGC 954 CAAGAAGGGCAGCACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGC 377 TITCIAIGCCAGICAGAIGGCICAACGGAAGAICCGAGACAICCIGGCCAAGGITAAGCA 737 77 AGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGCTCCTCCTATAGCTCCTTTATGCAGGC 378 ACCACCCGAAACACCCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGC ccaarricaaggcricagggaaggaarcrarggcaaacrcaaggaggaagricrrrggricc AGTACCAAGAGACCAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAATCATCGGACA AGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGCTGCTCCCTATAGGTCCTTTATGCAGGC TCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGCCCATCATCGG CCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCC AGTACCAAGAGCCCAGACCCCTGATGAGAACGACCAGGTCATCGTGAAATCATCGGACA TITCIATGCCAGTCAGATGGCTCAACGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCA GCAGCATCAGAAGGGACAGAGTAACCAGGCCCAGGCACGGAGGAAGTGACCAGCCCCTCC CGCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGA CAAGGAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGT 601 CCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGA TCACCTGATCCCTGGCCTGAACCTGCTGCTGTAGGTCTTTTCCCCAGCTTCATCCAGCGC Gaps Score 1085.4; DB 4; Length 1182; Pred. No. 3.9e-297; 0; Mismatches 6; Indels 6; Query Match
Best Local Similarity 98.9%;
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                                      858 GCCTGAGAATGAGTGGGAATCCGGGACACCTGGGCCGGGCTGTAGATCAGGTTTGCCCAC
                         GCCTGAGAATGAGTGGGAATCCGGGACACNTGGGCCGGGCTGTAGATCAGGTTTGCCCAC
                                                                             918 TIGATIGAGAAAGAIGITCCAGIGAGGAACCCIGATCICTCAGCCCCAAACACCCCA
                                                                                               1555 ATTGGCCCAACACTGTNTGCCCCTCGGGGTGTCAGAAATTNTAGCGCAAGGCACTTTTAA
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The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. vstemic lupus erythematosus, rheumatodid arthritis and multiple solerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, Dumonary disorders, cardiovascular disorders, (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atheroscierosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
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98.9%; Pred. No. 3.9e-297;
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RUBEN S M.
BARASH S C.
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TCACCTGATCCCTGGCCTGAACCTGCTGCTGTAGGTCTTTTCCCCAGCTTCATCCAGCGC
            TCACCTGATCCCTGGCCTGAACCTGGCTGTAGGTCTTTTCCCAGCTTCATCCAGGC
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RESULT 7 AAS26566 ID AAS26566 standard; cDNA; 1129

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Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac artest; cerebrovascular disorder; cerebral ischaemia; anglogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                               Seq ID 745
                                                                                                 Human cDNA encoding a novel secreted protein,
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24-FEB-2000; 2000US-0186369P.

26-MAR-2000; 2000US-0186350P.

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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to encoded secreted proteins. The nucleic acids and proteins are used to concern the condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a also be used in allowating symptoms associated with the disorders and in diagnostic manunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac carest, osrborvascular disorders e.g. cardiac carest, osrborvascular disorders e.g. Carebral ischaemia, analycenesis, nervous system disorders e.g. Alzhimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Company other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used to as used companitives, fat content, libid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present capabilities, fat content printional components. The present components of the printed sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
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              17-NOV-2000; 2000US-0249200F.
01-DEC-2000; 2000US-025030160P.
05-DEC-2000; 2000US-0251901P.
05-DEC-2000; 2000US-0251908P.
05-DEC-2000; 2000US-0251908P.
06-DEC-2000; 2000US-025190P.
06-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
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181 AGCAGCGTTACTGGGGCTGCTCCTTTATATGCTGCTCCCGAGCAGGAGATG

791 AGCAGCGTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATG

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disorder;
muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
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24-FEB-2000; 2000US-0114886P.
07-JUL-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0216647P.
11-JUL-2000; 2000US-0216680P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217487P.
11-JUL-2000; 2000US-0217487P.
14-JUL-2000; 2000US-0220947P.
14-JUL-2000; 2000US-0220947P.
14-JUL-2000; 2000US-0220948P.
14-JUL-2000; 2000US-0225568P.
14-JUL-2000; 2000US-0225568P.
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14-JUL-2000; 2000US-0225568P.
14-JUL-2000; 2000US-022568P.
15-JUL-2000; 2000US-022989P.
15-JUL-2000; 2000US-023689P.
25-SEP-2000; 2000US-023636P.
26-CT-2000; 2000US-02363998P.
26-CT-2000; 2000US-023636P.
27-SEP-2000; 2000US-023636P.
27-SEP-2000; 2000US-023636P.
28-SEP-2000; 2000US-023636P.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C
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                                                                                                                                                                                            The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated
                                                            1271 ATGGCTCAACGGAAGATCCGAGACATCCTGGCCCCAGGTTAAGCAGCAGCATCAGAAGGGA
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K, Kojima S, Otsuki T, Koga
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Wakamatsu A, Sugiyama T, Nagai
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human novel polypeptides and their associated bolymuclectides. The polypeptides and polymuclectides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. gastrointestinal disorders, pulmonary disorders, reproductive disorders, gastrointestinal disorders, bilmonary disorders, cardiovascular disorders, (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stager renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1150
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                                               New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1069.8; DB 7; Length
Pred. No. 1e-292;
3; Mismatches 5; Indels
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                                                                                                                                                                                                             Claim 1; SEQ ID NO 745; 402pp; English.
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98.7%;
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and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a CDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EDO
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                                                                                                                                                                      Sequence 833 BP; 223 A; 225 C; 215 G; 166 T; 0 U; 4 Other;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                    Score 732.8; DB 4;
Pred. No. 3.6e-197;
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated ben denotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for Synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length coinses were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from
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Pred. No. 3.6e-197;
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K, Kojima S,
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a T, Nagai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel isolated polypeptide (I) which comprising an imminogenic portion of a lung tumour protein or variant (P2) which have cytostatic activity. The polypeptides and polymolectides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polymuclectides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
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                    TCTTTTCCCAGCTTCATCCAGCGCAGTCCCGCCGCCTCCCAGCAGCGTTACTGGGGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                           fusion
                                                                                                                                                                                                                                                                                                         The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABU48959 to ABU49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAAATGCGGGGGCTGCTGAGAAGTCGATTACTATCCTCTCTACTCCTGAAGGCACCTC
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     Henderson R.
Fanger GR;
                                                                                                                                                                                 Polynucleotides encoding lung tumor polypeptides, useful for lung cancer or stimulating an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1740 BP; 526 A; 406 C; 417 G; 391 T; 0 U; 0 Other;
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  SX, Kalos MD,
, Marnerakis M,
Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 582.2; DB 6;
Pred. No. 2.8e-154;
0; Mismatches 433;
Skeiky YAW, Li SX
er N, Retter MW, I
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66.2%;
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Matches 858; Conservative
        Wang A, Ske
PD, Fanger N
:TS, Carter I
                                                                                                          WPI; 2002-090513/12.
P-PSDB; ABB74997.
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Mcneill I
Vedvick 7
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DB 6; Length 1740; T; 0 U; 0 Other;

Score 582.2; DB 6; Pred. No. 2.8e-154; 0; Mismatches 433;

Query Match 34.1%; Best Local Similarity 66.2%; Matches 858; Conservative (

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Sequence 1740 BP;

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522 IGGGCAGAGGGGCTCCTCAAGGCAGGGGTCTCCAGGATCCGTATCCAAGCAGAAACCATG 217 GGACATCCCCCTTCGGCTCCTGGTGCCCAGTATGTGGGGTGCCATTATTGGCAAGGA

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AGCCATCATGAAGCTGAATGGCCACCAGTTGGAGAACCATGCCCTGAAGGTCTCCTACAT

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SX, Kalos MD, Henderson RA;
Durham M, Fanger GR, Vedvick TS;
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Fanger N, Retter MW,
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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PD, Fange
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942 ATTGCAGGAATTGACGCTGTATAATCCAGAACGCACTATTACAGTTAAAGGCAATGTTGA 1001

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The present invention describes isolated human lung carcinoma polymucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polymucleotide that hybridises to the oligonucleotide and comparing the amount of polymucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in paramaceutical compositions, e.g. the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ02418 to ABQ02486 and ABB61866 to increase.
                                                                                                          Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.
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P-PSDB; ABP61917.
  Watanabe
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P-PSDB; ABB75054
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09-OCT-2000; 2
12-DEC-2000; 2
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02-AUG-2000; 2000US-00630940.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
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Pred. No. 2.8e-154;
0; Mismatches 433; Indels
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Retter MW, Marnerakis M,
Watanabe Y, Peckham DW;
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PD, Fanger N, Retter
TS, Carter D, Watanab
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Best Local Similarity 66.29
Marches 858; Conservative
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                                                                                                                                                                       tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                                                                                                                                     Human lung tumour L523S recombinant polynucleotide SEQ ID NO:447
                                                                                                     BP
                                                                                                  ABL49297 standard; cDNA; 1743
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                                                                                                                                      (first entry)
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Human; lung

Ното

01-MAY-2002

ABL49297

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The present invention describes human lung tumour proteins. Human lung tumour proteins and polynuclectides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynuclectides, antibodies, proteins, proteins, proteins, polynuclectides, antibodies, proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABH48959 to ABH49300 and ABH7496 to ABH75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        642 AGGTGCCACCATTCGGAACATCACCAAACAGACCCAGTCTAAAATCGATGTCCACCGTAA
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Pred. No. 2.8e-154;
0; Mismatches 433; Indels 6;
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Retter MW, Marnerakis M,
Watanabe Y, Peckham DW;
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A,Gene: CESP.MBB.5
A,Map position: 3
A,Introns: 38/3; 96/1; 133/3; 255/3; 307/3; 395/2; 436/2; 492/3; 657/3; 759/1; 820/1
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single-stranded nu
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oHisGlnGlnAsnGlnGlnHisGlnAlaGlyGlnHisGlnSerHisHisGlnSerGl 279
                 hypothetical prote
high density lipop
vigilin - chicken
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hnRNP protein E2 -
dC stretch-binding
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hypothetical prote
MHC class III hist
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glutenin high mole
MHC class III hist
probable RNA-bind:
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 Percent Similarity:
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-C=Cgn2 1/USF7C spool p/US09270437/runat 13072004 121922 9618/app_query.fasta_1.1863
-D=Cgn2 1/USF7C spool p/US09270437/runat 13072004 121922 9618/app_query.fasta_1.1863
-DE-ERR 78 -QFWT=fastan -SUBFIX-FPF -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -GTRAT=1 -END=-1 -WATRIX-blosum62 - NAJIGN=1b - MIGN=1b - MODE=LOCAL
-UNITS=bits -GTRAT=1 -END=-1 -WATRIX-blosum60 - ALIGN=1b - MODE=LOCAL
-UNITS=bits -GTRAT=1 -END=-1 - MATRIX-BLOSUM00000
-USPMT=pto -NORM-ext -HEAFSIZE=50 -MINTSH=0 -MAXLEN-2000000000
-NORM-FPF - NORM-ext -HEAFSIZE=50 -MINT -DSFBLOCK=100 -LONGLOG
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3110
1 agggacgctgccgcaccgcc.....atttccttcaggttttaaaa 1708
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Db 639 nGluPheLeuGluAspAsnAlaThrIleAsnSerSerAspAlaIleGluGluLysProLy 659	Qy 980GTTCGTATGGTATCATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCA 1029	Qy 1030 GGGAAGAATCTATGGGCAAACTCAAGGAGAGAAACTTTTGGTCCC 1075	Qy 1076AAGGAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGC 1125  Db 699 pGlyAspArgSerHisMetLeuArgIleArgThrGluValSerValProThrArgIleII 719	1126 TGGCCGGGTCATTGGCAAAGGTGGAAAACGGTGAACTTGCAGATTTGACGCCAGC	Qy 1186 TGAGGTGGTAGCAAGAGACCAGACCCCTGAT	Qy 1220GAGAACGACCAGGTCATCGTGAAAATCATGGACATTTCTATGCCAGTCAGT	1276 TCAACGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAGAAGGGACAGAG	Qy 1336 TAACCAGGCCCGGGAGGAAGTGACCAGCCCTCCCTGTCCCTTNGAGTCCAGGAC 1395 ::: Db 796 sArgAsnLysSerSerAspTyrLys	Oy 1396 AACAACGGCCAGAAATCGAGAGTGTGCTCTCCCCGGCAGGCCTGAGAATGAGTGGGAATC 1455	Oy 1456 CGGGACACNTGGGCCGGGCTGTAGATCAGGTTTGCCCACTTGATGAGAAAGATGTTCCA 1515	Qy 1516 GTGAGGAACCCTGATCTNTCAGCCCCAACCCCACCCAATTGGCCCAACACTGTNTGCC 1575	Oy 1576 CCTCGGGGTGTCA 1588	psis thalians	C, Date: UZ-Marz-ZUU1 #Sequence_revision UZ-Marz-ZUU1 #text_change 31-Mar-ZUU1 C, Accession: D96554 C, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; De	ansen, N.F.; Hughes, B.; Huzar, L. Nature 408, 816-820, 2000 A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M	Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.	A.Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: D96554 A;Status: preliminary A;Wolecule type: DNA	A;Residues: 1-621 <sto> A;Cross-references: GB:AE005173; NID:g11094762; PIDN:AAG29695.1; GSPDB:GN00141</sto>
151 CTCTCGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGCGGGGGCCCCCAGCCAAGCAGCA 210	GCAAGTGGACATCCCCTTCGGCTCCTGGTGCCCAC	CAGINICAMETATATAGCAAGAGGGGCCACATCGAAGAAACA  ::	GACCCAGTCCAAGATAGACGTGCATAGGAAGGAAGGAAACGCAGGTGC	AGCTGAAAAAGCCATCAGTGCACTCCACCCCTGAGGGCTGCTCTCTGCTGTTTAAGAT  NASNASPAKGI ELEUTHIVAA HASGI YVAI NAI AGII OA HANAABAAK		TCCCTGAAGATCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAAGGAAGG	526 GAACCTGAAGAAGGTAGAGAAGATACCGAGAAAAATCACCATCTCC 574 :::::   ::::	575TCGTTGCAAGACCTTAACCTTTACAACCCTGAGAGAC 612	CATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGGGCGGAGGAAATAATGAAATTGTTGCAGGCCGAGCAGGAAATAATGAAATTGTTGCAGGCCGAGCAGGAAATAATGAAATTGTTGCAGGCCGAGCAGGAAATAATGAAAATTGTTGCAGGCCGAGCAAGAATAATGAAAATAATGAAAAAAAA	GAAAGTTCGGAAGGCCTATGAGAATGATGTGGCTGCCATGAGCTCTCACCTG	-AICCTGGCCTGAACCTGCTGTAGGTCTTTTCCCAGCTTCATCAGCGCAGCGCAGCCGAGCCAGCGAGCG	GCCGCCTCCCAGCAGCGTTACTGGGGCTGCTCCCTAT	818 832 ::	833GCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGG 882	883 CGCCATCATCGGCAAGAGGGCAGCACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTC 942	943 CATCAAGATTGCACCACCCGAAACACCTGACTCCAAA	979 979 979 619 SATGLYSLEUASDGluThrAspSerGlyCysGluGlyValAlaSerGlyAspHisProGl 639	6
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J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Huizar, L.
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L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, F.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
Inalysis of chromosome 1 of the plant Arabidopsis.
                                                          -GITCGTATGGTTATCATCACTGGACCGCCAGAGGCCCCAATTCAAGGCTCA 1029
                                                                                                                                                                           CTATGGCAAACTCAAGGAGGAGAACTTCTTTGGTCCC------ 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1455
                                                                                                                                                                                                                                                                                         -AAGGAGGAAGTGAAGCTGGAGACCCACATACGTGCCAGCATCAGCAGC 1125
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uGluAspAsnAlaThrIleAsnSerSerAspAlaIleGluGluLysProLy 659
                                                                                                           rGluArgMetValThrIleAsnGlyAspAspLeuGlnLeuLeuLysAlaGl 679
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thaliana (mouse-ear cress)
quence_revision 02-Mar-2001 #text_change 31-Mar-2001
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|PheSerLysIleAlaGluThrSerSerSerLeuProSerSerGlyMetAs
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sileProGluGluGluArgAsnGlyGlyGluValTyrArgHisAspAspGl
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|Ser 847
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probable pre-mRNA splicing factor - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T41600
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
Submitted to the EMBL Data Library, October 1998
A;Reference number: 222003
A;Accession: T41600
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T41600
A;Readules: 1-388 cLNN
A;Residues: 1-388 cLNN
A;Residues: 1-388 cLNN
A;Residues: BMBL:AL031825; PIDN:CAA21234.1; GSPDB:GN00068; SPDB:SPCC757.09c
A;Experimental source: strain 972h-; cosmid c757
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------GluproSerAlaAlaValValAlaArgLeuLeuValHisSerProTyrIle 371
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| 412 ValGlnValIleGlyAsnLeu------LysThrValGlnAspAlaLeuPheGlnIle
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                                                                         ACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCCCAATTCAAG
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ValHisPheArgLeuLeuCysProAlaThrArgThrGlyAlaIleIleGlyLysGlyGly
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Matches:
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A,Gene: F19C24.19
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qq	88 ThrTyrAlaThrGlnGlnLeuThrLeuArgAlaLeuLeuSerThrArgGlu 104	0 6
δ	254 GIGGGIGCCATTATIGGGAAGGAGGGCCACCATCCCCAACATCACAAAACAGACCCAG 313	Na R
qq	105 AlaGlyileileileGlyLysAlaGlyLysAsnVaiAlaGluLeuArgSerThrThrAsn 124	
δλ	314 TCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTG 373	A)
qq	125 ValLysAlaGlyValThrLysAlaValProAsnValHisAspArgValLeuThrIle 143	AA
67	374 CACTCCACCCTGAGGCCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAA 433	AAA
QQ	144 SerGlyProLeuGluAsnValValArgAlaTyrArgPhellelleAspIlePhe 161	AAA
δλ	434 GAGGCTAAGGACACCAAAACGGCTGACGAGGTTCCC	A
qq	::::::   162AlaLysAsnSerThrAsnProAspGlyThrProSerAspAlaAsnThrProArgLys 180	, A
QY	470 CIGAAGAICCIGGCCCAIAAIAACTIIGIAGGCGICICAIIGGCAAGGAAGGACGGAAC 529	Al
QQ	181 LeuargLeullealaHisSerLeuMetGlySerIlelleGlyArgAsnGlyLeuArg 200	200
ογ	TCG	2 6 6
qa	201 ileLysLeulleGlnAspLysCysSerCysArgMetIleAlaSerLysAspMet 218	e d
δλ	590 ACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGG 649	-sn
qq	219 LeuProGlnSerThrGluArgThrValGluIleHisGlyThrValAspAsnLeuHisAla 238	٥٧
ò	650 GCCGAGCAGAAATAATGAAGAAGATCGGGAGGCCTATGAG	q <sub>O</sub>
DP	239 AlaileTrpGluileGlyLysCysLeuileAspAspTrpGluArgGlyAlaGlyThrVal 258	ζ
ζζ	CTGATC	q <sub>0</sub>
qa	259 PheTyrAsnProValSerArgLeuThrGlnProLeuProSerLeuAlaser 275	λō
δλ	746 GIAGGICITIICCCAGCITCAICCAGCGCAGICCCGCCGCCTCCCAGCAGCGIT 799	qu
ОЪ	276 ThrAlaSerProGlnGlnValSerProProAlaAlaProSerThrThr 291	ζ
δ'n	800 ACTGGGGCTGCT 823	qa
QΩ	::     292 SerGlyGluAlalleProGluAsnPheValSerTyrGlyAlaGlnValPheProAlaThr 311	δ
٥'n	824TITIAIGCAGGCICCCGAGCAGGAGAIGGIGCAGGIGITIAICCCCGCCCAG 874	ପ୍
Пр	312 GlnMetProPheLeuGlnGlnProLysValThrGlnAsnIleSerIleProAlaAsp 330	ð
δλ	875 GCAGTGGGCCCATCATCGGCAAGAGGGGCAGCACTCATCAAACAGCTCTCCCGGTTTGCC 934	셤
Ω	331 MetValdlyCysllelleGlyArgGlyGlySerLysIleSerGlulleArgArgThrSer 350	ò
δ	935 AGCGCCTCCATCAAGATTGCACCACCACAACACCTGACTCCAAAGTTCGTATGGTTATC 994	Ω
QC	351 GlySerLysIleSerIleAlaLysGluProHisAspGluThrGlyGluArgMetPheThr 370	ò
ζ	995 ATCACTGGACCGCCGAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAG 1054	ପ୍ର
qq	371 ileThrGlyThrHisGluGluAsnGluLysAlaLeuPheLeuLeuTyrGlnGlnLeuGlu 390	ò
δ	1055 GAGGAG 1060	qq
<del>Q</del>	391 MetGlu 392	ò
RESULT .		qq
hypother C, Specie	hypothetical protein [imported] - Arabidopsis thaliana C,Species: Arabidopsis thaliana (mouse-ear cress)	λ <sub>0</sub>

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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C$Accession: C$6275
R;Thocomic C$6275
R;Thocomic C$A.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Marure 408, 816-820, 200
Rature 408, 816-820, 200
Rature 408, 816-820, 200
R; Hudhors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, R.; Marzio, M.; Rooney, T.; Rowley, D.; Sakano, H.
RATZO, M.; Rooney, T.; Rowley, D.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, cer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
Rythle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
RyAccession: C$6275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 AlaLeuProGlyCysGluGluArgValValThrMetTyrSerThrAsnGluGluLeuAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 GGGGCCACCATCCGCAACATCACAAAACAGACCCCAGTCCAAGATAGACGTGCATAGGAAG
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200 LeullelleGlyGluProLeu-----
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	US-09-270-437D-5 (1-1708) x T27855 (1-768)  QY 131 GGGCGCCGAGGGGCTTTGGCTCTCGGGGTCAGCCCCGCCAGGGCTCACCTGTGGCAGG 190	Db 224 GlyAlaAspGlyGlyIleGlyThrLeuLysArgProLeuAspSerGluIleLeuAsp 242	191 GGGGCCCCAGCCAAGCAGCAGCAA	Db 243 GIYABPLeuileProThrLysLysSerSerGiuValGiyAspLeuAsnMetGiyAspSer 262 Qy 215GIGGACAICCCCTICGGCICCTGGIGCCAGIAIGIGGGIGCCATI 265	Db 263 AspLysIleThrAspIleTyrProValProGluLysValValGlyLeuVal 279  Qy 266 ATTGGGAAGGAGGGGCCCACCATCCGGAACATCACAAAACAGACCAGGCCAGTCCAAGATAGAC 325	Db 280 IleGlyLysGlyGlyGerGluIleArgLeuIleGlnGlnThrSerGlyCysArgValGln 299	Qy 326 GTGCATAGGAAGGAAGGTGCAGCTGAAAAGCCATCAGTGTGCACTCCACCCCT 385   :  :: :: :: :: :: :: :: :: :: :: :: ::	386 GAGGCTGCTCCCCCTTGTAAGATGATCTTGGAGATTATGCATAAGAG	Db 320 AspGlnValAlaValAlaArgGlnMetIleThrGlnValIleAsnArgAsnGlnThrGly 339  Qy 437 GCTAAGGACACCAAAACGGCTGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTT 496	Db 340 AlaGinProGlyAlaAlaProGlyGluValThrGluGluMetLeuileProAlaAspLys 359	Qy 497 GTAGGGCGTCTCATTGGCAAGGAAGGAACGGAACCTGAAGAAGGTAGAGCAAGATACCGAG 556 ::::   :::    ::::::::::::::::::::::	557 ACAAAAATCACCATCTTCCTCGTTGAAGACCTTTACCTTTACCAACCCTT	Db 380 LeuArgAsnCysAsnValValGlnGluThrThrThrAlaThrGlyGlnProLysPro 398	605 GAGAGGACCATCACTGTGAAGGGGCCCATCGAGAATTGTTGCAGGCCCGAGCAGGAAATA	DD 399 DEUARGMELIEGIYSEFFICALAALAILEGIUINFALADEUVAIHISASHIIE 418 OV 665 ATGAAGAAGTTCGGGAAGGCCTATGAGAATGAGGCGTGCCATGAGCCTCTCACCTGATC	 	Qy 725 CCTGGCCTGAACCTGGCTGTGTAGGTCTTTTCCCAGCTCCAGCGCAGTCCCGCCG 784		Qy 785 CCTCCCAGCAGCGTTACTGGGGCTCCCTATAGCTCCTTTATGCAGGCAG	435 GlnProSerGlyGlnPheGlyGlyTyrGlyAlaGlnGluAlaGlnAlaLysGly	Db 454GluvalileValProArgLeuSerAlaGlyMetileIleGlyLysGlyGly 470	905 CAGCACATGAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCGAA	471	Qy 965 ACACCTGACTCCAAAGTTCGTATGGTTATCATGCACTGGACCGCCAGAGGCCCAATTCAAG 1024  [	1025 GCTCASGGAAGAATCTATGGCAAACTCAAAGGAGGAGAACTTCTTGGTCCAAG		Oy 1079 GAGGAAGTGAAGCTGGAGACC
Db 228 HisLeu237	Oy 776 GICCCGCCCTCCCAGCAGCGTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAG 832	200 Methibutioning Company Com	258 AlaValArgArgAsplieAlaAspAlaArgGluPheCysValCysPheIleCysProAla	Qy 872 CAGGCAGTGGGCCATCATCGGCAAGAAGGGCAGCACATCAAACAGCTCTCCCGGTTT 931 ::        ::	932 GCCAGCGCCTCCATCAAGATTGCACCACCGGAACACCTGACTCCAAAGTTCGTATGGTT	DD 298 INFGLYALATNFILEARGYALASNFNFSSERGIUTHFASPASPASPASPCysile 315 QV 992 ATCATCACTGGACCGCCAGAG		OY 1022 AAGGCTCAGGGAAGAATCTATGGCAAACTCCAAGGAGGAGAACTTCTTTGGTCCCAAG 1078 :::	Qy 1079 GAGGAAGTGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCACCTGGCCGGGTCATT 1138	1139 GGCAAAGGTGGAAAAAGGGTGAAGTTGAAGTTTGACGGCAGCTGAGGTGGTA		Qy 1196 GTACCAAGAGACCAGACCCGGATGAGAACGACCAGGTCATCGTGAAAATCATC 1249  TO 1::::::::::::::::::::::::::::::::::::	ייייי באייייייייייייייייייייייייייייייי	410 GlySerProAspAlaAlaMetLysAlaLeuThrGlnVallIeleuArgueu	Qy 1310 AAG 1312		RESULT 5 T27855	hypothetical protein ZK418.9 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans	)	submitted to the EMBL Data Library, April 1994 A; Description: The sequence of C. elegans cosmid ZK418.	A; Neterion: Induce:: 220430 A;Accession: T2785 A;Status: preliminary; translated from GB/EMBL/DDBJ	A; Molecule type: DNA A; Residues: 1-768 <ful> A; Cross-references: EMBL: U00047; PIDN: AAA50693.1; CESP: ZK418.9</ful>	A;Experimental source: strain Bristol N2 C;Genetics:	A;Gene: CESP:ZK418.9 A;Introns: 166/1; 221/3; 243/1; 279/1; 387/3; 490/1; 567/3; 727/2	6.59e-10 Length:	Matches: Conservative:	2.00%

71 AACCATGCCCTGAAGGTCTCCTACATCCCCGATGAGCAGATAGCACAGGGACCT 124	: : :           : :	TyrLysValProAspGlyMetValGlyPheIleIleGlyArgGlyGluGlnIleSer AACATCACAAAACAGACCCAGTCCAAGATAGACGCAGGAGGAGAACGCAGGTGCA AACATCACAAAAACAGACCCAGTCCAAGATAGACGCATAGGAAGGA	144 ProdlukrgSerCysMetLeurhrGlyThrProdluServalgInSerAlaLysArgLeu 163 413 ATCTTGAGATTATAAGAGGCTAAGACCAAAACGGCTGAC 460 ::: :::   :::         164 LeuAspGlnIleValGluLysGlyArgProAlaProdlyPheHisHisGlyAspGlyPro 183 461GAGGTTCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCTCTCATTGGCAAG 517	GAAGGACGGAACCTGAAGAAGGAAGAAACCGAGACAAAAATCACCATCTCCTCG	623 AAGGGGCCATCGAGAATTGTTGCAGGACCGAGGAAATAATGAAGAAAGTTCGGGAG 682  [	728 GGCCTGAACCTGGTGTGTAGGTCTTTTCCCAGCTTCATCCAGCGCGGTCCCGCCGCT 787 269	277 GlylleAspValProllePloArgPheAlaValGlylleVall
8 8 8 8	a & a &	6 8 5 8 5	8 8 8 8	3 6 8 6 8	8 6 8 6	Levens, Qy trream e Db Qy Qy Qy	유 충 유 충 유 ·
531 AspArgGlySerAlaGlyThrValLeuProGlyGlnSerIlePheTyrMetHisValPro 1115 GCATCAGCAGCTGGCAGGTCATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAAT	Oy 1232 GTGTGGGAATCATGGGAATTTGTATGCGAGTGAGTGGCTGA 1279 S90 LysValPheGluIleLysGlySerGlnLeuGlnIleHisHisAlaSerHisLeuValArg 609 Oy 1280 GGGAAGATGCGAGACATC	Qy         1297           Db         630 GlyTyrGlnGlnGlnGlnAlaMetPheSerAlaGlyThrGlnAsnGlyGlyTyrGlnSer 649           Qy         1298CTGGCCCAAGGTAAAGCAGCAGCATCAGAAGGACT 1336           Bb         650 ThrGlyGlyPheileGlnGlnGlnGlnGlnGlnPhedlnHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	670 AlaProGlaAsnGly-GlyGlyValGlaAsuFueuProThrGluMetTyrGlaAsnPr 1397 ACAACGGCACAAATCCAGACTGTGCTCTCCCCGGCAGG :::	70 148 148 72 72 153	DD 748AsnThrAlaProLeuGlyAspValSerGlyValProGin 760 RESULT 6 A53184 myc far upstream element-binding protein - human N:Alternate names: FUSE-binding protein C;Species: Homo sapiens (man) C;Date: 06-03an-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999	Charces Dev. 8, 465-480, 1994  Ribuncan, R.; Bazar, L.; Michelotti, G.; Tomonaga, T.; Krutzsch, H.; Avigan, M.; Levenn Genes Dev. 8, 465-480, 1994  A./iltle: A sequence-specific, single-strand binding protein activates the far upstream A./Reference number: A53184; MUID:94170991; PMID:812529  A./Scatus: preliminary  A./Molecule type: mRNA  A./Residues: 1-644 eDUN>  A./Residues: 1-644 eDUN>  A./Cross-references: GB:U05040; NID:9460151; PIDN:AAR17976.1; PID:9460152	Alignment Scores: Pred. No.: Pred. No.: Score: Scor

QY 1019 TTCAAGGCTCAG 1030         ::     Db 334 HisalaAlaGlulleIleThrAspLeuLeuArgSerValGlnAlaGlyAsnProGlyGly 353   Qy 1031GGAAGAATCTATGGCAAACTCAAGGAGAAACTTCTTGGTCCAAG 1078	A; Residues: 1-680 <sch> A; Cross-references: EMBL: U88174; PIDN: AAB42272.1; GSPDB:GN0019; CESP:MO1A10.1 A; Experimental source: strain Bristol N2; clone M01A10 C; Genelics: A; Gene: CESP: M01A10.1</sch>
 354 ProglyProglydlyArgglyArgglyArgglyGlnGlyAsnTrpAsnMetGlyProPro 3	A;Map position: 1 A;Introns: 63/2; 97/3; 121/1; 160/1; 269/3; 411/3; 512/1; 649/2
1079 GAGGAAGTGGAAGCCCACATACGTGCCAGCATCAGCAGCTGGCCGGGTCATT 113:	ment Scores: No.: :: tit Similarity:
QY 1139 GGCAAAGGGGGGAACAACGGGGGGGGGGGGGGGGGGGG	arity: 20.50* mismacones: 7.73* Indels: 2 Gaps:
Qy 1199 CCAAGAGACCGGAGAGAGGACGACCAGGTCATGTGAAAATCATGGGACAT 1255	US-09-270-437D-5 (1-1708) x T25832 (1-680) Qy 104 GAGCAGATAGCACAGGGACCTGAGAATGGGCGCCGAGGGGGGCTTTGGCTCTCGGGGGTCAG 163
Qy 1256CGAGACAGTCAGATGGCTCAACGGAAGATCCGAGACAT 1296	:::     :::
Db 433 ProGlnGlnIleAspTyrAlaArgGlnLeulleGluGluLys1leGlyGlyFroValAsn 452	Qy         164 CCCCGCCAGGGCTCACCTGTGGCAGCGGGGGCCCCAGCCAAGCAGCAGGAGTG 217
1	116GluGlySerAspGluTyrGluGluTyrAlaProProCysLy
CCTTNGA	AspileAspTyrArgValAspThrSerThrThrVallleLysAlaSerValSerllePro
	Qy 245 ACCCAGTATGTGGGTGCCATTATTGGCAAGGGGGGCCACCATCGCAACATCACAAAA 304
Qy 1387 GTCCAGGA 1394	Db 154 GluGluSerValGlyLeuValIleGlyArgAsnGlyValGluIleGlnAlaIleSerGln 173
Db 490 snProGlyProProGlyProAlaProHisGlyProProAlaProTyrAlaProGlnGlyT 510	Qy         305         CAGACCCAGTCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAGCC 364
510 rpGlyAsnAlaTyrProHisTrpGlnGlnAlaProProAspProA	365 AICAGIGCACTCCACCCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTT
TAGATCAC	bb 193 ValAspIleTyrGlyIleSerGluAsnIleGluValAlaLysLysEusIleAsnGluVal 212
Db 526 laLysAlaGlyThrAspProAsnSerAla-AlaTrpAlaAlaTyrTyrAla 542	4 4
OY 1492 CACTTGATTGAGAAAGATGTTCCAGTGAGGAACCCTGATCTNTCAGCCCCAAACACCCCA 1551  Db 543 Historycyclndlnglnala	Db 213 ValalaArgGlyArgLysLeuSerGlnGluProLeuProCysSerValProGlnPheGln 232 Oy 443GACACCAAAACGGCTGAGGATTCCCCTGAAGATCCTGGGCCCATAATAAC 493
1552 CCAATTGGCCCAACACTGTNTGCCCCTCGGGGTGTCAGAAATTNTAGCGCAAGGCAC 16	233 ProllePr
	Qy 494 TTTGTAGGGGGTCTCATTGGCAAGGAAGGACGGAACCTGAAGAAGGTAGAGGAAGGTAGAGC 553
1609 TTTTAAACGTGGATTGTTTAAAGAAGCTCTCCAGGCCCCACCAAGAGGGTGGATCACAC 16	253 LysCysGlyAlaileileGlyLysCysGlyGluGlnMetArgLysLeuArgSerTrpThr
DD 571	Oy 554 GAGACAAATCACCATCICCTCGIIGCAACACCITIACAACCCIITACAACCCIIGAAGAGACACC 613  DD 273 ASHCVSASDPhelleLeuIleGinGlukshAshIleAlaspSerVallySPro 290
:::    :::     584 LysAlaTrpGluGluTyrTyrLysLysMetGlyGlnAlaValProAlaProThrGly	ATCACTGTGAAGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGAATI
RESULT 7	Db 291 LeuGlnIleThrGlyGln
hypothetical protein M01A10.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 15-Oct-1999	Qy 674 GITCGGGAGGCCIATGAGAATGATGTGGCCTGCCATGAGCTCTCACCTGATCCCTGGCTG 733
1	AACCTGGCTGCTGTAGGTCTTTTCCC
submitted to the EMBL Data Library, February 1997 Ny Description: The sequence of C. elegans cosmid MO1A10.	Db 315 AspGluCys
;Reference number: Z20094 ;Accession: T25832 ;Status: preliminary; translated from GB/EMBL/DDBJ	794 AGCGTTACTGGGGCTGCTCATAGCTCCTTTATGCAGGCTCCCGAGCAGAGAGAG
Molecule type: DNA	Db 321 GlyMetAlaGlyAsnSerProValAlaAlaMetSerLeu 333

us-09-270-437d-5\_1.rpr

Qy         64 GTTGGAGAA	Qy 175 CTCACCTGTGGCAGCGGGGCCCCAGCCAAGCAAGTGGACATCCCCCTTCG 231		406 TAAGATCTTGGAGATTATGCATAAAGAGGCTAAGGACCC	217 yGlyGlyGlyArgArgMetGlyGlyGlnAlaGlyAlaAspGlnPheValMetLySile 481 GGCCCATAATAACTTTGTAGGCGTCTCATTGGCAAGGAAGG	Qy 541 AGAGGAAGATACCGAGACAAAATCACCATCTCCTCGTTGCAAGACCT 588	Oy 649 GGCCGAGCAGAAATAATGAAGATCGGGAGGCCTATGAGAATGATGATGGCTGCCAT 708	769 CAGGGAGTCCCGCGCCTCCCAGCAGCGTTACTGGGGCTGCTCCTATAGCTCCTTTAT 320 yGlyTyrGlnAlaArgProProSerSerTrp-AlaPro-Pro	Qy 829 GCAGGCTCCCGAGCAGAGAGAGGTGTTTATCCCCGCCCAGGCAGT 879	534 FIGELOSIIIYIGAYOLINSEEFIOOYIGAYSEELYIFIOOLINGIIINIESEEFALGAGIYIYE 913CAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCACCACCCGAAAC
854 CAGGIGITTATCCCCGCCCAGGCGCCCTCATCGCCAAGAAGGGCCACCATC	3/4 LeumetGlluArginrLeuvalVallieGlyAsnLysAsnLysValTyrValCysAla 1034 AGAATCTATGGCAAACTCAAGGAGAAACTTCTTTGGTCCCAAGGAGGAAGTGAAGCTG	DD 413PheRyrMetLeulleProAlaSerLysCysGlyLeuVallleGlyArgGlyGlyGly 431  Qy 1154 ACGGTGAACGAGTTGCAGAATTTGACGCCAGCTGAGGTGCTAGTACCAAGAGAC 1207  DD 432 ThrIleArgGlnileAsnLysGluSerGlyAlaTyrCysGluMetSerArgAsp 449  RESULT 8  T02627	hypochetical protein At2g55960 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein T19L18.23 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001 C;Accession: T02827; H84654. R;Rounsley, S.D.; Raul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,	:	A;Cross-references: EMBL:ACO04447; NID:93413696; PID:93413716 A;Experimental source: cultivar Columbia A;Experimental source: cultivar Columbia R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.	A; Accession: H04654 A; Status: preliminary A; Molecule type: DMA A; Cross_references: GB: AE002093; NID: g3413716; PIDN: AAC31239.1; GSPDB: GN00139 C; Genetics: T19L18.23; At2025960	A;Map position: 2 A;Introns: 112/1; 206/3; 264/3; 304/3 C;Superfamily: glutenin Alignment Scores:	d. No.: re: cent Sim t Local ry Match	US-09-270-437D-5 (1-1708) x T02627 (1-632)  OY 4 GACGCTGCCGCACCGCCCCAGTTTACCCCGGGAGCCATCATGAAGCTGAATGGCCACCA 63  OY 1

158 GGTCGCCCGCCAGGGCTCACCTGTGGCGGGGGCCCCAGCCAAGCAGCAG  19 SerArgbrodinSerAspTyrAspAspAsndlydlySerLysArgdryargTyrArgdlyAsp  212	198 LeulleGlnileSerGlyGluValLeulleValLysLysAlaLeuLeuGlnileAlaser 217  671 AAAGTTCGGGAGGCCTATGACAATGATGTGGCTGCCATGAGCTCTCACCTGATCCTGGC 730  218 ArgleuHisGludan	y 1010 GAGGCCCAATTCAAGGCAGAAGAATCTATGGCAAACTCAAGGAGGAAACTTCTTT 1069
6       8	S.; re	₹ 60 ° 60 ° 60 ° 60 ° 60 ° 60 ° 60 ° 60
	hetical protein F8M21.160 - Arabidopsis thaliana cies: Arabidopsis thaliana (mouse-ear cress) cies: Arabidopsis thaliana (mouse-ear cress) cies: Arabidopsis thaliana (mouse-ear cress) acies: Arabidopsis thaliana (mouse-ear cress) assion: T49962 an, M. Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, erence number: 224493 ession: T49965 ession: T49966 ession: T5966 ession: T496 ess	US-09-270-437D-5 (1-1708) x T49962 (1-568) Qy 98 CCCGARGAGCAGAATAGCACAGGGACCTGAGAATGGCCCCCAAGGGGCTTTGCCTCTCGG 157               :::::::: Db 3 ProAspHisArgMetSerProAspHisArgAspSerHisArgLysArg 18

569 ATCTCCTCGTTGCAAGACCTTACCCTTACAACCCTGAGAGGACCATCACTGTGAAG 625 168 LeuValGlnAspAsnGlnSerValSerAspGlnSerLySProleuArglleThr 185 626 GGGGCCATCGAGAATTGTTGCAGGCCGAGGAGGAGGAGGAGGCC 685	GCTGCTCCCTATAGCAGGCTCCCAGGCAGAGATGGTGAGGTGTTTATC G1yG1yG1yAlaSerAlaArgG1yG1yAlaSerAlaArgG1yG1yAlaSerAlaArgG1yG1yAlaSerAlaArgG1yG1yAlaSerAlaArgG1yG1yAlaSerAlaArgG1yG1yAlaJalaArgG1yG1yAlaJala	294 LeuvāliysLysSerThrMetGlnGlnGlyGlyGlyGlyGinValnaladijyalawetVal 313  1082 GaAGTGAAGCTGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCGGTCATT 1138  314 SerAsnGlualaSerThrPheTyrMetSerValProAlaAlaLysCysGlyLuvuJille 333  1139 GGCAAAGGTGGAAAAAGGGTGAAGTTGCAGGAATTTGCAGGCTGTGAGGTGGTAGTA 1198  314 SerAsnGlualaSerThrPheTyrMetSerValProAlaAlaLysCysGlyLuvuJille 333  1139 GCAAAGGTGGAAAAAAGGGTGATGAGAATTGCAGGCGCTGAGGTGGTGTAGTA 1198  314 GlyLysGlyGlyGlyThrIleLysGlnIleAsnSerGluSerGlyAlaHisCysGluLuv 353  1139 CCAAGAGCCCAGACCCCTGATGAGAACGACCAGGTCATCGTGGCTGAGTGTGTGAGTGTGAGTGA
6 6 6 6 6 6 6	6 8 6 8 6 8 6 6 6	6 2 4 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6
	RESULT 10 T19217-6 T19217-6 T19217-6 T19217-6 T19217-6 T19219 C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Cac-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C.Accession: T19216 R.McMurray, A. Submitted to the EMBL Data Library, June 1996 A.Reference number: Z19092 A.Accession: T19216 A.Accession: T19216 A.Residues: T19216 A.Residues: 1-589 -WIL> A.Gress-references: EMBL:Z73969; PIDN:CAA98232.1; GSPDB:GN00023; CESP:C12D8.1a A.Gress-references: EMBL:Z73969; PIDN:CAA98232.1; GSPDB:GN00023; CESP:C12D8.1a A.Greence: CESP:C12D8.1a A.Residues: 7/3; 25/1; 159/3; 318/3; 513/2	Alignment Scores:    8.86e-09   Marches: 589     8.86e-09   Marches: 106     8.86e-104   18.75\$   Mismatches: 122     9.86e-104   18.75\$   Mismatches: 120     19.09-270-437D-5 (1-1708) x T19216 (1-589)     19.7 CCAGCCAAGCAGCAAGCAAGCACACCCCCTT

::: ThrValAlaAlaThrThrProThrValAspProValThrGlyGluGlnAspTyrSer 505	15			TTTAAAGAAGCTCTCCAGCACCAACAAGAGGTGGATCACACCTCAG 1672	.::	is CL troop	18: 8.95e-09 Length: 611 232.00 Matches: 108 1ity: 37.15% Conservative: 106 Ilarity: 18.75% Mismatches: 232 7.46% Indels: 130 2 Gaps: 18	-5 (1-1708) x T19217 (1-611)	CCAGCCAAGCAAGCAAGTGGACATCCCCCTT	CGGCTCCTGGTGCCCACCCAGTATGTGGCGTGCCATTATTGGCAAGGGG 280 :::	GCCACCATCCGCAACATCACAAACAGACCCAGTCCAAGATAGACGTGCATAGGAAGGA	AACGCAGGIGCAGCIGAAAAGCCATCAGIGIGCACTCCACCCCTGAGGGCTGCTCTCC 400 ::: AspproSerSerGlyValArgMetValThrLeuGluGlySerArgSerAsnValGluThr 129	GCTTGTAAGATGATGAGATTATGCATAAAGAGGCTAAGGACACCAAA 451	ACGCTGACGAGGTICCCCTGAGGATCCTGGCCCATAATAACTTIGTAGGGCGTCTC 508	ATTGGCAAGGAAGGACGGAACCTGAAGAAGGTAGAAGAAACGAGGACAAAAAATCACC 568
::: ThrValAla	CAATIGG	AladinTrp	AlaGlnMet	TTTAAAGAA(	1	rotein CI: -1999 #see -1999 #see -1927 -19	res: arity: milarity:	Ŋ						ı Dı	
486	1553	206	1586	1625	546	ILT 11 the control of	Alignment Scores: Pred. No.: Scores Percent Similarity: Best Local Similarity: Query Match:	19-270-437D-	197	230	281	341	401	452	509
d d	ò	QQ	& <u>8</u>	ò	QQ	REST T1192C C) SP C) SP C) SP C) AC C) AC C) AC A) AC A) AC A) AC C) GE C) GE C) GE C) GE C) GE C) AC C) GE C) AC C) GE C) AC C) AC	Alig Prec Scor Perc Best Quer DB:	0-SU	δς Q	\$ g	55 임	\$ G	& 원	SS GS	Sy of

ъ . q	569 A	ATCTCCTCGTTGCAAGACCTTACCCTTTACAACCCTGAGAGGACCATCACTGTGAAG 625 ::: :::
> Q	208	GGGGCCATCGAGAATTGTTGCAGGCCGAGCAGGAAATAATGAAGAAGTTCGGGAGGCC 685
ъ д	686	TATGAGAATGATGTGGCTGCCATGAGCTCTCACCTGATCCCTGGCCTGAACCTGGCTGCT 745
*	9	CAICCAGGGCAGICCCGCGGCTCCCAGCAGCGITACTGGG 80
Ω	241 /	
> 4	806 (	GCTGCTCCCTATAGCTCCTTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATC 865
a ≽-	99	SCAAGAAGGGCAGCACATCAAACAGCTCTCC 92
. ہ	26	  ProArgSerSerValG1y11e11eG1yLysG1nG1yAspThr11eLysArgLeuAla 275
<b>≯</b>	926	CGGITTGCCAGCGCCTCCATCAAGATTGCACCCGAAACACCCGGACTCCAAAGTTCGT 985
۾	276 1	MetGluThrGlyThrLyslleGlnPheLysProAspAspAspProSerThrProGluArg 295
<b></b> ⊁	986	0
ą	296	CysalaValileMetólyThrArgAspGlnIleTyrArgAlaThrGluArgIleThrGlu 315
<u>.</u>	1046	AAACTCAAGGAGGAGAACTTCTTTGGTCCCAAGGAG 1081
.Q	316	LeuValiysiysSerThrMetGlnGlnGlyGlyGlyGlyAsnValAlaĠlyAlaMetVal 335
<u>۸</u> .	20 0	TGAAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATT 11
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<u>≯</u> : -	99	1 1
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≿ £	99	CCAAGAGACCAGACCCCTGATGAGAACGACCAGGTCATCGTGAAA 1243
ρ;	9 5	51 DUE
<u>ب</u> و	396	, m
٨	1304	CAGGITAAGCAGCAGCATCAGAAGGGACAGAGTAACCAGGGCCCAGGGCAGGAAGTGA 1363
.g	414	asi:
≵:	1364	CCAGCCCCTCCCTGTCCCTTNGAGTCCAGGACAACAACGGGCAGGAAATCGAGAGTGTGCT 1423
ą	430	::: SeralaProAlaGlnAsnAsnPheGlyGlyGlnGlnGlnTrpAsnProValAlaGln 448
<b>*</b>	1424	Ã.
đ	449	roalaalaalaginasnProTyrGinValGiyGiyTrpGinGinAsnS
<i>\</i> 2	1460	ACACNIGGGCCGGGCIGIAGAICAGGITG 1489
ą	469	nGlnThrAlaAlaProAl
≿	1490	CCCACTTGATTGAGAAAGATGTTCCAGTGAGGAACC 15
q	489	507
ζζ	1526	CTGATCTNTCAGCCCCAAACACCCACC1552

Page 12

ArglleLysGlnThrLeuProSerSerProThrThrThrLysSerSerProSerAspPro CTGAAGATCCTGGCCCATAATAACTTTGTAGGCGT	1 (2) P	566 ACCATCTCCTCGTTGCAAGACCTTACCAACCTTACAACCTTGAAGAGACCACCATGAAGAGACCTTGAAGAAGACCTTAACAACCTTAAAACCTTAAAACCTTAAAACCTTAAAACCTTAAAAACCTTAAAAACCTTAAAAACCTTAAAAACCTTAAAAACCTTAAAAAA	626 GGGCCATCGAGAATTGTTGCAGGGCCGAGCAGGAAATAATGAAGAAAGTTCGGGAG	Db 228 GlyGluProGluGlnAsnArgLysAlaValGluLeulleileGlnLyslleGlnGluAsp 247 Qy 683	248 ProglnSerGlySerCysLeuAsnIleSerTyrAlaAsnValThrGlyProValAlaAsn	Qy 695GATGTGCCATG 709  Db 268 SerAsnProThrGlySerProTyrAlaAsnThrAlaGluValLeuProThrAlaAlaAla 287	AGCTCTCACCTGATCCCTGGCTGAACCTGGCTGTAGGTCTTTTCCCA	092	Db 308 SerGlyPheThrGlyAsnAspLeuValAlaIleThrSerAlaLeuAsnThrLeuAlaSer 327	Qy         761	OY 776 GTCCGCCGCCTCCCAGCAGCGTTACTGGGGCTGCTCCCTATAGCTCCTTTATGCAGGCT 835 ::::::::::::::::::::::::::::::::::::	836 CCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCCCAGCCAG	368 TyralaSerdlu	QY 896 AAGAAGGGCACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAGATTGCA 955	QY 956 CCACCGGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCC 1015	Qy 1016 CAATTCAAGGCTCAGGGAAGATCTATGGCAAACTCAAGGAGGAGAACTTC 1066	QY 1127 GGCCGGGTCATTGGCAAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCT 1186	OY 1187 GAGGTGGTAGTACCAAGAGACCAGACCCCTGATGAGAACGACCAGGTCATGGTG 1240	AAAAICATCGGACATTCTATGCCGGTCGAA 1279
:::	AlaGinTrpMetGluTyrTyrLysSerIleGlyAlaHisAspLysAlaGluAlaValGluTCAGAAATTNTAGCGCAAGGCACTTTTAAACGTGGATTG :::	8 AlaGlnMetLysLysLysLysLysLysLysLy	568IleGlnGlnMetProMetGlyMetAlaMetProGln 579	nn-1 - human (man)	. vo-sep-1990 #sequence_revision 06-sep-1996 #text_change 05-Nov-1999 ssion: 13846g anovich, R.J.; Posner, J.B.; Darnell, R.B.	oplastic Ri Antiger 19; MUID:94000830; E	A;Accession: 134489 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-510 <res></res>	S.references: EMBL:U04840; NID:g440877; PIDN:AAA16022.1; PID:g440878 tics: : Nova-1	Alignment Scores:	4.92e-08 Length: 221.50 Matches: 1milarity: 34.89\$ Conservati: Similarity: 71.64\$ Mismarhoo	7.12% Mismacches: 7.12% Indels: 2 Gaps:	370	125 GAGANTGGCCGCCGAGGGGCTTTGGCT-CGGGGTCAG 163 :::         :::		1ATCCCCTTGGCTCCTGGTGCCACCAGTATGTGGGTGCCATTATTGGCAAGAG GINTYFPHellenIveVillenIII =:	### ##################################	3 CCTGAGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCAT  Vol G VAL	AAAGAGGCTAAG	129 ASNVALALALYSTNrGLUProValSerIleLeuGlnProGlnThrThrValAsnProAsp 148 443

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evolutionarily conserved motif
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|LeuArgLeuValValProAlaThrGlnCysGlySerLeuIleGlyLysGlyGlyCysLys 119
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80 GluGluAspIleAsnSerSerMetThrAsnSerThrAlaAlaSerArgProProValThr 99
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A; Molecule type: mRNA,
A; Molecule type: mRNA,
A; Residues: 1-204, 'V, '206-356 <1EF>
A; Residues: 1-204, 'V, '206-356 <1EF>
A; Cross-references: ENBL:X78137; NID:9460770; PIDN:CAA55016.1; PID:9460771
A; Experimental source: AMA cells (transformed human amnion cells)
A; Experimental source: AMA cells (transformed human amnion cells)
B; Note: submitted to the EMBL Data Library, March 1994
B; Asashaim, H.C.; Loukianova, T.; Deggerdal, A.; Smeland, E.B.
Nucleic Acids Res. 22, 959-964, 1994
B; Mulb:94203810; PMID:8152927
B; Reference number: 843489; MulD:94203810; PMID:8152927
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AjResidues: 125-139;251-265;315-323 <KI2>
AjResidues: 125-139;251-265;315-323 <KI2>
Exp. 13. Edechem. 230. 453, 1995
Bur. J. Blochem. 230. 453, 1995
AjTitle: Characterisation of two major cellular poly(rC)-binding human proteins, AjReference number: 865678; MUID:95331278; PMID:7607214
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|AlaGlyValThrGluSerGlyLeuAsnValThrLeuThrlleArgLeuLeuMetHisGly
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A;Cross-references: EMBL:Z29505; NID:g444020; PIDN:CAA82631.1; PID:g444021
                                                                                »x protein 1 - human
names: nucleic acid-binding protein; protein PCBP-1
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A,Cross-references: GDB:344947
C,Keywords: RNA binding
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us-09-270-437d-5\_1.rpr

ble RNA-binding protein - Arabidopsis thaliana ernate names: protein T32N21.30 cies: Arabidopsis thaliana (mouse-ear cress) e: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000 ession: T46439 an, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; I H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. tited to the Protein Sequence Database, March 2000 ession: T48439 1169 CAGAATTTGACGGCAGCTGAGGTGGTAGTACCAAGAGCAGACCAGACCGATGAGAACGAC 1228 1229 CAGGICAICGIGAAAAICAICGGACAITITCTAIGCCAGICAGAIGGCTCAACGGAAGAIC 1288 344 ArgHisGluSerGlyAlaSerIleLysIle-----AspGluProLeuGluGlySerAsp 361 260 GCCATTATTGGCAAGGAGGGGCCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAG 319 535 374 CACTCCACCCCTGAGGGCTGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAA 433 88 SerGlySerIleLysGluValValValAsnGlyLeuGluLeuIleLeuAspLysLeuHisSer 107 47 48 SerVallleGlyLysGlyGlySerThrIleThrGluPheGlnAlaLysSerGlyAlaArg 67 320 ATAGACGTGCATAGGAAGGAGAAC----GCAGGTGCAGCTGAAAAGCCCATCAGTGTG 373 434 GAG-----GCTAAGGACACCAAAACGGCTGACGAGGTTCCC-------CTGAAG 475 87 ||| ::: ||| 28 AlaAspSerAlaGluLysProThrHisIleArgPheLeuValSerAsnAlaAlaAlaGly 1289 CGAGACATCCTGGCCCAGGTTAAGCAGCAGCATCAGAAGGGA 1330 382 GlnAsnSerValLysGlnPheSerGluAspTyrAlaTyrGly 395 ission: T48439

us: preliminary

coule type: DNA

coule type: DNA

seriesences: EMBL:AL162875

rimental source: cultivar Columbia; BAC clone T32M21 313 80 62 113 76 position: 5 oons: 29/1; 108/3; 144/2; 209/1; 229/3; 261/3; 282/2 :: T32M21.30 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 270-437D-5 (1-1708) x T48439 (1-313) 185 GCAGCGGGGCCCCA----1.51e-07 214.00 42.90% 24.17% 6.88% t Similarity: ocal Similarity: Match: ent Scores: No.: 200

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959 CCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCCCAA 1018
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                    145 SerPhelleGluGluSerLysAlaGlylleLysIleSerProLeu---AspAsnThrPhe 163
                                                                 596 TACAAC---CCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGGGCC 652
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Davis-Smyth T., Duncan R.C., Zheng T., Michelotti G., Levens D.;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 3 (FUSE binding protein 3)
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Result

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                                                                                                                                                                                 364
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                          185 GCAGCGGGGCCCCAGCCAAGCAGCAGCAAGTGGACATCCCCCTTCGGCTCCTGGTGCCC 244
                                                                                                                                                                                                                                                                                              144
                                                                                                                                                                                                                                                                                                                                                             :::
145 ValAspArgCysArgAsnGlyProGlyPheHisAsnAspIleAspSerAsnSerThrIle 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||||||
321 IleLeuThrAlaGlnGluArgAspGlyPheGlyGlyLeuAlaAlaAlaArgGlyArg--- 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAIGIGGCIGCCAIGAGCICTCACCIGAICCCIGGCCIGAACCIGGCIGCIGIAGGICIT 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 ThrTyrThrValProAlaAspLysCysGlyLeuVallleGlyLysGlyGlyGlyAsnIle 377
                                                                82
                                                    245 ACCCAGINIGIGGGIGCCATINITIGGCAAGGAGGGGCCACCATCCGCAACATCACAAA
                                                                                                                             CAGACCCAGTCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAGCC
                                                                                                                                                                                                               106 GluSerGlyCysLysileGlnIle---AlaSerGluSerSerGlyIleProGluArgPro
                                                                                                                                                                                                                                                                                  ||||
|181 GlyGlyThrIleLysGlnLeuGlnGlyArgThrGlyValLysMetValMet-----
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199 IleGlnAspGlyProLeuProThrGlyAlaAspLysProLeuArgIleThrGlyAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||||||| :::|||||||::: ||||||::
264 AlaValGlyIleValIleGlyArgAsnGlyGluMetIleLysLysIleGlnAsnAspAla
                                                                                                                                                                                                                                                                                                                                  -----CATAAAGAGGCTAAGGACACCAAAACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                         458 GACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTAGGGCGTCTCATTGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                 518 GAAGGACGGAACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATCACCATCTCCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              578 TTGCAAGACCTTACCCTT---TACAACCCTGAGGAGCATCACTGTGAAGGGGGCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGTGGGCGCCATCGGCAAGAAGGGGCAGCACATCAAACAGCTCTCCCGGTTTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 AspPheArgGlyValArgGlyAspPhe----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---GlyArgGlyArgGlyAspTrpSerValGlyAlaProGlyGlyValGln---GluIle
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                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KH 1.
KH 2.
KH 3.
KH 3.
KH 4.
MABLVQGQSAPVGMKABGFVDALHRVRQIAAKIDSIPHLNN
STPLVDPSVYGYGVQKRPLDDGV -> MPPI (in
                                                                                                                                                                                                                                                SIMILARITY: Contains 4 KH domains.

ACMTION: Ref.1 sequence differs from that shown due to a frameshift in position 18.

CAUTION: Ref.2 (AAH01135) sequence differs from that shown due to a frameshift in position 527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerAlaProValGiy------MetLysAlaGluGlyPheValAspAlaLeuHisArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 GAGAACCATGCCCTGAAGGTCTCCTACATCCCCGATGAGCAGATAGCACAGGGACCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| ||| |||:::
27 ArgGlnIleAlaAlaLysIleAspSerIleProHisLeuAsnAsnSerThrProLeuVal
                                            far-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWART, SM00322; KH; s.

PROSITE; PS50084; KH TYPE 1; 4.

Transcription regulation; Trans-acting factor; Nuclear protein;

DNA-binding; Repeat; Alternative splicing.
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: May interact with single-stranded DNA from the jupstream element (FUSB). May activate gene expression.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing; Named isoforms=2;
Name=1;
                                                                                                                                                                                         Isoid=096124-2; Sequence=VSP 008323; VSP 008324;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Detected in a number of cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP 008323.
Missing (In isoform 2).
/FTId=VSP 008324.
V - D (IN REF. 1).
W; F1BE223542BC197D CRC64;
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1129
90
220
1147
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 AGTITACCCCGGGGAGCCATCATGAAGCTGAATGGC
                                                                                                                                                       IsoId=Q96I24-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U69127; AAC50893.1; ALT FRAME.
EMBL; BC001325; AAH01325.1; ALT_FRAME.
EMBL; BC007874; AAH07874.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR004087; KH dom.
Interpro; IPR004088; KH rype_1.
Pfam; PP00013; KH; 3.
SYART; SM00322; KH; 3.
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61640 MW;
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264.00
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22.01$
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317
421
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Best Local Similarity:
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253
354
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DOMAIN
VARSPLIC
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1160 AACGAGTIGCAGAATTIGACGGCAGCTGAGGTGGTAGTACCAAGAGACCCAGACCCCCTGAT 1219
                                                                                                                                                                                                                                                                                                                                                     .352 CGGAGGAAGTGACCAGCCCCTCCCTGTCCCTTNGAGTCCAGGACAACAACGGGCAGAAAT 1411
                                                                                                                                                                                                                                                                                         425 ValGlyGlyThrAsnLeuGlyAlaProGlyAlaPheGlyGlnSerProPheSerGln--- 443
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MEDINE-2238257; PubMed-12477932;

MEDINE-2238257; PubMed-12477932;

MEDINE-2238257; PubMed-12477932;

MEDINE-2238257; PubMed-12477932;

MACHANGER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

MALSchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MACHANGO L., Machan R., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roback S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.W., Sodergran E.D., Lu X., Gibbs R.A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Tuckman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                           378 LysSerIleAsnGlnGlnSerGlyAlaHisValGluLeuGlnArgAsnProProProAsn 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         497
                                                                                                                                                                                                                     405 PheThrileArgGlyValProGlnGlnileGluValAlaArgGlnLeuileAspGluLys 424
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10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last snnotation update)
Far upstream element binding protein 1 (FUSE binding protein 1) (FBP).
                                                                                        1220 GAGAACGACCAGGTCATCGTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAA
                                                                                                                                                                                                                                                                  ---GGACAGAGTAACCAGGCCCAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                         1412 CGAGAGTGTGCTCTCCCCGGCAGGCCTGAGAATGAGTGGGGAATCCG------
                                                                                                                                                                            1280 CGGAAGATCCGAGACATCCTGGCCCAGGTTAAGCAGCAGCAGCATCAGAAG-----
                                                                                                                                                                                                                                                                                                                                                                                             -----proproAlaProProHisGlnAsnThrPheProProArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GGACACNTGGGCCGGGCTGTAGATCA
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| 17 ||SerGlyProProAlaPheLeuThrGlnGlyJrpGlySerThrTyrGlnAlaTrpGlnGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                  SerAsp-----
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MININGERIOR OF 1.286 FROW N.A. ISODORNE 3).

MININGERIOR CONTRACTOR N. Manubase T., Adachi J., Sono H., Kondo S., MININGERIOR C., Control N. Manubase T., Adachi J., Scholbach C., Golobori T., Baldarelli M., Charry V., Hesegway W., Nogami A., Scholbach C., Golobori T., Baldarelli M., Manubase T., Manubase T., Charry R., Manubase T., Manubase T., Charry R., Manubase T., Manubase T., Charry R., Manubase T., Charry R., Manubase T., Manubase T., Farerer K., Goline S., Dalla E., Forger M., Frazer K. S., Charry R., Manubase T., Manubase T.
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265	CysclinhisalaAlaGiuileIleThrAspLeuLeuArgSerValGlnAlaGlyAsnPro- CysclinhisAlaAlaGiuileIleThrAspLeuLeuArgSerValGlnAlaGlyAsnPro- GGAAGGAACTCAAGGAACTCAAGGAGGAACTCAAGGAGGACTGCCG GIVGLyProGlyProGlyGlyArgGlyGlyGlyBrandargCCGCGG GTCATTGCCAAAGGAGAAAACGGGGAAACTCAAGGAGGTGGCCG GTCATTGCCAAAGGAGAAAACGGGGAGAAATTCAAGGCGGGGCGG GTCATTGCCAAAGGAGAAAAACGGGAGAAATTCAAGGCGGGGGGGG	1603 AGGCACTITIAAACGTGGATTGTTTAAAGAGCTCTCCAGGCCCCACCAAGAGGGTGGAT 1662
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DOMAIN DOMAIN DOMAIN VARSPLIC CONFLICT SEQUENCE ignment Scor ed. No.: rcent Simila st Local Sime erry Match:	99 SEGGCACCACTTCGAGAACCATCCCTAAAGGTCTCCTACATCCCCATGACCAGIIS Db 19 GlyclyglyvalvalAshaspAlaPheiyeAspAlaLeuclnArgalaArgGInileAla 38 116 CAGGGACCTGAGAATGGCCGCCGAGGGGCTTCGCGTCTCGGGGGG 175 117 CAG	Qy 722 AICCCIGACCIGACCIGCTGTAGGICITITCCCAGCTICAICCAGCGCAGICCCG 781

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------TCAGTGGGAAGAAAATAAAATTTCCTTCA 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=22388257; PubMed=12477932;
MEDINE=22388257; PubMed=12477932;
MEDINE=22388257; PubMed=12477932;
MEDINE=22388257; PubMed=12477932;
MEDINE=22388257; PubMed=12477932;
MAISTOR R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Marmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Boraldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uodin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W., Villalon D.K., Muzry D.W., Sodergren E.J., Lu X., Gibbs R.A., Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Mixera M.A., Ratisus D.E., Schmutz J., Marra M.A., Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                             :::|||
578 TyrThrLysAlaTrpGluGluTyrTyrLysLysMetGlyGlnAlaValProAlaProAla 597
                                                                                                                                                                                                                                                                                                                                                                                                                     far
                                                                                                                                             FUBI_HUMAN STANDARD; PRT; 643 AA.
096AB4; 01288;
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
(DNA helicase V) (HDH V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE OF 45-64; 133-145; 271-283; 308-321; 379-386; 414-424 AND
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1), SEQUENCE OF 191-193; 203-206; 272-279; 284-290; 300-314; 321-328; 394-397; 409-411; 430-438 AND 440-443. AND FUNCTION.

TISSUE-Leukemia;

MEDLINE=94170991; PubMed=8125259;

Duncan R., Bazar L., Michelotti G., Tomonaga T., Krutzsch H., Avigan M., Levens D.;

A sequence-specific, single-strand binding protein activates the upstream element of c-myc and defines a new DNA-binding motif.";

Genes Dev. 8:465-480(1994).
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vindigni A., Ochem A., Triolo G., Falaschi A.;
"Identification of human DNA helicase V with the far upstream
element binding protein.";
Nucleic Acids Res. 29:1061-1067(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22166132; PubMed=12176931;
Rappsilber J., Ryder U., Lamond A.I., Mann M.;
"Large-scale proteomic analysis of the human spliceosome.";
Genome Res. 12:1231-1245(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE, AND MASS SPECTROSCOPY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21127960; PubMed=11222755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 2).
            1663 CACACC----
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22716800, PubMed=12819782;

Kim M.J., Park B.-J., Kang Y.-S., Kim H.J., Park J.-H., Kang J.W.,

Lee S.W., Han J.M., Lee H.-W., Kim S.;

"Downregulation of FUSE-binding protein and c-myc by tRNA synthetase
cofactor p38 is required for lung cell differentiation.";

Nat. Genet. 34:330-336(2003).
                                                                                  interacting repressor targets TFIIH to inhibit activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=096AE4-2; Sequence=VSP 008321;
Note=No experimental confirmation available;
-!- PIM: Ubiquitinated. This targets the protein for proteasome-
INTERACTION WITH SIAHBP1.
MEDLINE=20337922; PubMed=10882074;
Liu J., He L., Collins I., Ge H., Libutti D., Li J., Egly J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50084; KH TYPE_1; 4.
Transcription regulation; Trans-acting factor; Nuclear protein;
DNA-binding; Repeat; UDl conjugation; Alternative splicing;
3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQ -> CRFDPASIELAL (in isoform 2).
FTIG=VS 008321.
Q -> QS (IN REF 1).
086D4EAAOACF807B CRC64;
                                                                                                                                                                     INTERACTION WITH JTV1, UBIQUITINATION, AND PROTEASOME-MEDIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q96AE4-1; Sequence=Displayed;
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-!- SIMILARITY: Contains 4 KH domains.
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KH 2.
KH 3.
KH 4.
GLY-RICH.
GLY-RICH.
PRO-RICH.
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InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_Cype_1.
Pfam; PF00013; KH; 4.
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EMBL; BC017247.1; -.
PDB; 1J4W; 06-MRA-02.
Genew; HGNC:4004; FUBP1.
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67473 1
                                                                                                         transcription.";
Mol. Cell 5:331-341(2000)
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                                                                                     "The FBP
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1004 CCGCCAGAGGCCCCAATTCAAGGCTCAG	lyarggly TGGAGACC	367 TrpAsnMetGlyProProGlyGlyLater:GluPheAsnPheileValProThrGly	1121 GCAGCIGGCGGGICAILGCCAAAGGIGGAAAAAGGGGGAAAAAAGGGGIGCAGGAAIILGACG IIG 1121	Qy 1181 GCAGCTGAGGTGGTAGTACCAAGAGCCGGGCCCTGATGAGAACGACCAGGTCATC 1237	1238 GTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAACGGAAG 1	Qy 1286 ATCGGAGACATCCTGGCCCAGGTTAAGCAGCATCAGAAGGACAGGA 1335		Qy 1374CCTGTCCCTTNGAGTCCAGGA	Oy 1395	Qy 1414 AGAGTGTCTCTCCCGGGAGGCCTGAGAATGAGTGGGAATCCGGGACACNTGGGCCGGG 1473	Qy 1474 CTGTAGATCAGGTTTGCCCACTTGATTGAGAAAGATGTTCCAGTGAGGAACCCTGATCTN 1533 :::        Db 539 TyrTyrAlaHisTyrTyrGlnGlnGlnAla548	Qy 1534 TCAGCCCCAAACACCCACCCAATTGGCCCAACACTGTNTGCCCCTCGGGGTGTCAGA 1590	QY 1591 AATTNTAGCGCAAGGCACTTTTAAACGTGGATTGTTTAAAGAAGCTCTCCAGGCCCCACC 1650 ::: ::	Oy 1651 AAGAGGTGGATCACCC	Qy 1687 AAATTTCCTTCAGGT 1701  Db 597 ProAlaProThrGly 601	RESULT 4 NOA2 HUMAN TO AC Q9UNW9; 043267; Q9UEA1; 492 AA.	DT 10-0CT-2003 (Rel. 42, Created) DT 10-0CT-2003 (Rel. 42, Last sequence update) DT 10-0CT-2003 (Rel. 42, Last annotation update) DE RNA-binding protein Nova-2 (Neuro-oncological ventral antigen 2)
Alignment Scores: Pred. No.: Pred. No.: Score: 247.50 Matches: Percent Similarity: 27.80% Conservative: 97 Best Local Similarity: 22.33% Mismatches: 202 Query Match: 196% Gaps: 32	ນປປນນັ້ນ	73 ProAspAlaLysLysValAlaProGlnAsnAspSerPheGlyThr 8	Oy 155 CGGGGTCAGCCCGCCAGGGCTCACCTGTGGCAGCGGGGGGCCCCAAGCAGCAGCAACAACAA 214 :::       ::: B8 GlnLeuProProMetHisGlnGlnGlnGlnArg 97	OY 215 GTGGACATCCCCCTTCGGCTCCTGGTGCCCAGTATGTGGCAAG 274	Oy 275 GAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGG 334	Qy 335 AAGGAGAACGCAGGTGCAGATGAAAAAGCCATCAGTGCACCCCTGAGGGCTGC 394 :::::	TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACC 4	Oy 449 AAAACGCTGACGAGGTTCCCCTGAAGATCCTGGCCCATAATAACTTTGTA 499  Db 1.77 HisHisGlvBrGlvBrGlvBrGlvBrGlvBrGlvBrGlvBrGlvBr	500 GGGCGTCTCATGGCAAGGAAGGACGGAACCTGAAGAAGGTAGACAAGATACCGAGAAC 55	AAAATCACCATCTCCTCGTTGCAAGACCTTACCACCTGAGAGAGCGC III:::    :::    ::     LV8MetValMet11eGlnAspGlvProGlnAspThrGlvAla	ATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGGGCCGAGCAGCAGAATA :::	Oy 665 ATGAAGAAAGTTCGGGAGGCCTATGAGAATGATGTGGCTGCCATG 709  1::::::::::   :::     251 LeuGluLeuIleArdAspGlnGlyGlyPheArgGluValArdAsnGluTyrGly 268	CATCC	770 AG	830 CAGGCTCCCGAGCAGAGATGGTGCTTTTATCCCCGCCCAGGCAGTGGCCGTC 88 274AsnGluGlyIleAspValProlleProAxgPheAlaValGlyIleVal 28	Oy 890 ATCGGCAAGAAGAGCACACATCAAACAGCTCTCCCGGTTTGCCAGCGCCTCCATCAAG 949	Oy 950 ATTGCACCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGA 1003

InterPro; LEAVOULUS; KH. 3.
PEGNART; SM00322; KH. 3.
PROSITE; PS50084; KH TYPE\_1; 3.
PROSITE; PS50084; KH TYPE\_1; 3.
Antigen; Nuclear profein; RNA-binding; Repeat; 3D-structure.
DOWAIN 10 26 BIPARTITE NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

A -> R (IN REF. 1). PAA -> TAT (IN REF. 1). 41B63EAF6899256B CRC64;

MW.

49008

CONFLICT

CONFLICT

KH 1.
KH 2.
ALA-RICH.
GLY-RICH.
KH 3.

99 196 405 393 247

32 130 232 332 406

DOMAIN DOMAIN DOMAIN DOMAIN 492 118 62 1185 15

Length: Matches: Conservative: Mismatches:

6.8e-08 236.50 37.89% 24.84% 7.60%

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores:

No.:

Indels:

U70477; AABB8661.1; ALT\_INIT.

EMBL; AF083898; AAC72355.1; -EMBL; AC006540; AAD13116.1; -PDB; 1DTJ; 18-FEB-00.
PDB; 1EC6; 07-APR-00.
Genew; HGNC, 7887; NOVA2.
MIM; 601991; --

InterPro; IPR004087; KH dom. InterPro; IPR004088; KH\_type\_1

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SECUENCE OF 29-492 FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J., Liu S.,

Ardix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,

Artix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,

Artix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,

Artiano A., Brower A., Sanders C., Ow D., Nolan M., Trong S.,

Kobayashi A., Olsen A.S., Carrano A.V.;

Sequence analysis of a 1.9 Mb region in 19913.2 between APOB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence specific RNA binding by a Nova KH domain: implications for paraneoplastic disease and the fragile X syndrome."; cell 100:323-3323(2000).

-!- FUNCTION: May regulate RNA splicing or metabolism in a specific subset of developing neurons (By similarity). Binds single strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 405-491 IN COMPLEX WITH RNA. MEDLINE=20139984; PubMed=10676814; Lewis H.A., Musunuru K., Jensen K.B., Edo C., Chen H., Darnell R.B., Burley S.K.;
                                                                                                                                                                                         Louis D.N.;
                                                                                                                                                   TISSUB-Brain;
MEDLINE-20197319; PubMed=10735272;
MEDLINE-20197319; PubMed=10735272;
Weki K., Ramaswamy S., Billings S.J., Mohrenweiser H.W., Louis D.N.;
"ANOVA, a putative astrocytic RNA binding protein gene that maps to chromosome 19q13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: Brain. Expression restricted to astrocytes.
DOMAIN: The third KH domain (KH3) recognizes specifically 5'-
                                                        Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 405-480.
MEDLINE=99148126; PubMed=10368286;
Lewis H.A., Chen H., Edo C., Buckanovich R.J., Yang Y.Y.-L.,
Musuntu K., Zhong R., Darnel B., Burley S.K.;
"Crystal structures of Nova-1 and Nova-2 K-homology RNA-binding
                                                                                                                                                                                                                                                                                                      MEDLINE=99007301; PubMed=9789075;
Yang Y.Y., Yin G.L., Darnell R.B.;
"The neuronal RNA-binding protein Nova-2 is implicated as the autoantigen targeted in POMA patients with dementia.";
Proc. Natl. Acad. Sci. U.S.A. 95:13254-13259(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
(Astrocytic NOVA1-like RNA-binding protein) NOVA2 OR ANOVA OR NOVA3.
                                                                                                                                                                                                                                                 Neurogenetics 1:31-36(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structure 7:191-203(1999).
                                          fomo sapiens (Human)
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                     SEQUENCE FROM N.A.
                                                                              Mammalia; Euther
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domains.";
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valThrvalSerGlyGluProGluGlnValHisLysAlaValSerAlaIleValGlnLys 199
                                      152 TCTCGGGGGCCCCCCCCAGGGCTCACCT-----GTGGCAGCGGGGGCCCCAGCCAAG 205
                                                                                                                                                                                                               266 ATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGAC 325
                                                                                                                                                                                                                                                                                                    326 GIGCATAGGAAGGAGAAC-----GCAGGIGCAGCIGAAAAAGCCAICAGIGIGCACICC 379
                                                                                                                                                                                                                                                                                                                                                                                      ACCCCIGAGGGCIGCICCICCGCIIGIAAGAIGAICIIGGAGAIIAIGCAIAAAGAGGCI 439
                                                                                                                                                                                                                                                                                                                                                                                                                               88 ThrAlaGluAlaLeuAsnAlaValHisSerPheileAlaGluLysVal---ArgGluIle 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 ProGlnAlaMetThrLysProdluValValAsnIleLeuGlnProGlnThrThrMetAsn 126
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8 SerArgLysArgFroLeuGluThrProProGluValValCysThrLysArgSerAsnThr
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US-09-270-437D-5 (1-1708) x NOA2_HUMAN (1-492)
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DISEASE: Autoantigen in the paraneoplastic opsoclonus myoclonus araxia (POMA), a paraneoplastic neurological syndrome/disorder (PNS/D) associated with breast cancer, fallopian cancer, and SCLCa and characterized primarily by loss of inhibitory control of motor neurons in the spinal cord and brainstem. Recognized by the 1gG autoantibody ANNA-2 (also called anti-Ri).

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                                                                                                                                                       GlyvalGlyalaPheProAlaAlaLeuProAlaPheSerGlyThrAspLeuLeuAlaIle 279
                   |||:::|||
|ValGinGluAspProGlnSerSerCysLeuAsnIleSerTyrAlaAsnValAlaGly 219
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                                                                                                                                                                                                                       835 TCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAGGCAGTGGGCGCCCATCATCGG 894
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       ---GCCTATGAGAAT----
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Last annotation update)
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[1] -SEQUENCE FROM N.A., SEQUENCE OF 104-119; 242-267; 679-685; 705-711 AND

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

Gallus gallus (Chicken)

NCBI\_TaxID=9031;

Gallus.

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743-766, FUNCTION, DEVELOPMENTAL STAGE, AND SUBCELLULAR LOCATION.
MEDLINE=21640447; PubMed=11781334;
Gu W., Pan F., Zhang H., Bassell G.J., Singer R.H.;
Gu W., Pan F., Zhang H., Bassell G.J., Singer R.H.;
A predominantly nuclear protein affecting cytoplasmic localization of beta-actin mRNA in fibroblasts and neurons.";
J. Cell Biol. 156:41-52(2002).
-!- FUNCTION: Binds to a 54-nuclectide localization signal (the zipcode) found in the 3' untranslated region of beta-actin mRNA and may play a role in its localization.
-!- SUBCELLULAR LOCATION: Predominantly nuclear. Also detected in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---AlaGluArgGly------ArgArgProProProAlaLeuThrGlyGlyAla
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                                                                                                                                                                                                                                             cytoplasm.
DEVELOPMENTAL STAGE: The highest expression is found in 6-d
embryos, is reduced to 30% before hatching and remains stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 TGGGCGCCGAGGGGGCTTTGGCTCTCGGGGTCAGCCCCGCCAGGGCTCACCTGTGGC
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GO; GO:0005634; C:Cytoplasm; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0003730; F:mRNA 3' UTR binding; IDA.
GO; GO:0008298; P:mRNA 1 oralization, intracellular; NAS.
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH_type_1.
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                                                                                                                                                                                                                                                                                                                     thereafter. SIMILARITY: Contains 4 KH domains.
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21.41%
7.57%
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Best Local Similarity:
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Pred. No.:
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                                                                        "Cooperative assembly of an hnRNP complex induced by a tissue-specific homolog of polypyrimidine tract binding protein."; Mol. 20:7459-7479(2000).

1. FUNCTION: Binds to the dendritic targeting element and may play a role in mRNA trafficking (By similarity). Part of a ternary complex that binds to the downstream control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in transcripts that are subject to tissue-specific alternative splicing. May interact with single-stranded DNA from the far-upstream element (FUSE). May activate
                                                                                                                                                                                                                                                                                                  and HNRPH1.

SUBCELLUIAR LOCATION: Nuclear. A small proportion is also found in the cytoplasm of neuronal cell bodies and dendrites (By similarity).
                                                                                                                                                                                                                                                                                   Part of a ternary complex containing FUBP2, PTBP1, PTBP2
                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Detected in neural and non-neural cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 4 KH domains.
CAUTION: Ref.3 sequence differs from that shown due to numerous
FUNCTION, AND INTERACTION WITH PIBP1; PTBP2 AND HNRPH1.
MEDLINE=20459250; PubMed=11003644;
Markovtsov V., Nikolic J.M., Goldman J.A., Turck C.W., Chou M.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00322; KH; 4.

PROSITE; PS50084; KH_TYPE_1; 4.

PROSITE; PS50084; KH_TYPE_1; 4.

Transport; mRNA transport; mRNA processing; mRNA splicing;
Transcription regulation; Trans-acting factor; Nuclear protein;
DNA-binding; RNA-binding; Repeat.
DOMAIN 233 299 KH 1.
DOMAIN 233 299 KH 3.

DOMAIN 322 386 KH 3.

Transcription regulation; Transcription; Transcription
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ALA/GLY/PRO-RICH.
G -> V (IN REF. 2).
V -> G (IN REF. 2).
G -> G (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
W, E07588DE438CA8B6 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, U94832; AAB5322.1; -.
EMBL, AF033747; AAD29861.1; -.
EMBL, AF093745; AAD29861.1; JOINED.
EMBL, AF093748; AAD29862.1; -.
EMBL, U69126; AAC50892.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH type_1.
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692 V
694 G
707 72709 MW;
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234.50
32.93%
21.75%
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SMART; SM00322; KH; 4.
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SUBUNIT: Part o
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MIM; 603445;
                                                             Black D.L.;
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Percent Similarity: Best Local Similarity: Query Match: DB:

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183
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|168 nLys1leGlnGlnAspSerGlyCysLysValGlnIleSerProAspSerGlyGlyLeu-- 187
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                                                                                                                                                                                                                                                                                                157 GGGTCAGCCCGCCA------
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US-09-270-437D-5 (1-1708) x FUB2_HUMAN (1-707)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified an or profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=22120219; PubMed=12124753;

Rumar D.V., Nighorn A., & John P.A.;

Rumar D.V., Nighorn A., & John P.A.;

Role of Nova-1 in regulating alpha2N, a novel glycine receptor

T Role of Nova-1 in regulating alpha2N, a novel glycine receptor

T Plice variant, in developing spinal cord neurons.";

J. Neurobiol. $2:156-165 (2002).

J. Neurobiol. $2:156-165 (2002).

J. Dinding pre-mRNA in a sequence-specific manner to activate exon inclusion. It binds specifically to the sequence UCAUY (By similarity). Acts to regulate a novel glycine receptor alpha-2 chain splice variant (alpha-2N) in developing spinal cord.

C chain splice variant (alpha-2N) in developing spinal cord.

SIMILARITY: Contains 3 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnAsnGlyThrHisThrGlyValProlleAspLeuAspProProAspSerArgLysArg
                                                Chordata, Craniata, Vertebrata, Buteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AY262017; AAP20872.1; ...
InterPro; IPR004089; KH_dom.
InterPro; IPR004088; KH_type_1.
Pfam; PF00013; KH; 3.
SWART; SW06322; KH; 3.
PROSITE; PS50084; KH TYPE 1; 3.
Antigen; Nuclear profein; RNA-binding; Repeat.
DOMAIN 26 42 (POTENTIAL).
                                                                                                                             STRAIN=BDIX, TISSUE=Cerebellum,
Knudsen A., Monstad S.E., Vedeler C.A.;
Nova-1, the paraneoplastic Ri antigen, is associated with breast
cancer.";
                                                                                                                                                                                                         Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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106
71
175
134
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Mismatches:
Indels:
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Matches:
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KH 2.
ALA-RICH.
KH 3.
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231.00
36.42%
21.81%
                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Choro
Mammalia; Eutheria; Rode:
NCBI_TaxID=10116;
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Best Local Similari
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Fragment).
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                                          CCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGTGGAAAAACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGGCCCAGGCACGGAGGAAGTGACCAGCCCCTCCCTGTCCCTTNGAGTCCAGGACAAC
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432 sLysCysGlyLeuValIleGlyArgGlyGlyGluAsnValLysAlaIleAsnGlnGlnTh
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                  CACTGGACCGCCAGAGGCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGA
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                                                                                                                                                                            ::: ||||||| ::: ||||||| eAspValProValProValPySerGlyGluMetIl
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
protein Nova-1 (Neuro-oncological
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                                                         GAGAAC-----GCAGGTGCAGCTGAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGC 391
                                                                                       LysAspPheTyrProGlyThrThrGluArgValCysLeuIleGlnGlyThrIleGluAla 107
                                                                                                                  TGCTCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGACACCAAA 451
                                                                                                                                                108 LeuAsnAlaValHisGlyPheIleAlaGluLysIleArgGluMetProGlnAsnValAla 127
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LysAlaValGluLeuIleIleGlnLysIleGlnGluAspProGlnSerGlySerCysLeu 226
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1088 AAGCTGGAGACCCACATACGTGTGCCAGCATCAGCAGCTGGCCGGGTCATTGGCAAAGGT 1147
                                                                                                                                            GGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCTGAGGTGGTAGTACCAAGA--- 1204
                                                                                                                                                                                                                                                                                         ---GACCAGACCCCTGATGAGAACGACCAGGTCATCGTGAAAATCATCGGACATTTCTAT 1261
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                                                                                                                                                                                                                                                                                                                                            Rehbein M., Wege K., Buck F., Schweizer M., Richter D., Kindler S.;
"Molecular characterization of MARTAL, a protein interacting with the dendritic targeting element of MARTAL, a protein interacting with the dendritic targeting element of MARTAL, a protein interacting with the J. Neurochem. 82:1039-1046(2002).

-I- FUNCTION: Part of a ternary complex that binds to the downstream control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in transcripts that are subject to tissue-specific alternative splicing. May interact with single-stranded DNA from the faruspiram element (FUSE). May activate gene expression (By similarity). Binds to the dendritic targeting element and may play a role in mRNA trafficking.
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--- SUBDNIT: Part of a ternary complex containing FUBP2, PTBP1, PTBP2 and HNRPH1 (By similarity).
--- SUBCELLULAR LOCATION: Nuclear. A small proportion is also found in the cytoplasm of neuronal cell bodies and dendrites.
--- SIMILARITY: Contains 4 KH domains.
                                                  400 Glu------IleAlaValProGluAsnLeuValGlyAlaIleLeuGlyLysGly
                                                                                                                                                                                               416 GlyLysThrLeuValGluTyrGlnGluLeuThrGlyAlaArgIleGlnIleSerLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 73-87; 89-108 AND 475-486, SUBCELLULAR
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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10-OCT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 2 (FUSE binding protein 2)
type splicing regulatory protein) (KSRP) (MAP2 RNA trans-acting protein 1) (MARTAI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1262 GCCAGTCAGATGGCTCAA 1279
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InterPro; IPR004088; KH_type_1.
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10-OCT-2003 (Rel. 42, Last seq
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LOCATION, AND FUNCTION.
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FUBP2 OR KHSRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preferentially to oliging do.
SUBCELLUIAR LOCATION: Loosely bound in the nucleus. May shuttle between the nucleus and the cytoplasm.
TISSUE SPECIFICITY: Abundantly expressed in skeletal muscle, thymus and peripheral blood leucocytes while a lower expression is beserved in prostate, spleen, testis, ovary, small intestine, heart, liver, adrenal and thyroid glands.
PTM: PHOSPHORYLATED. THE NON-PHOSPHORYLATED FORM(S) EXHIBITED THE STRONGEST POLY(RC)-BINDING ACTIVITY.
SIRNIARITY: Contains 3 KH domains.
CAUTION: There is probably a frameshift error in the nucleotide sequence of Ref.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-Lymphocytes,
MEDLINE-94203810; PubMed-8152927;
MEDLINE-94203810; PubMed-8152927;
Mashaim H.-C., Loukianova T., Degerdal A., Smeland E.B.;
"Tissue specific expression and cDNA structure of a human transcript encoding a nucleic acid binding [oligo(dC)] protein related to the pre-mENA binding protein K."
Nucleic Acids Res. 22:959-964(1994).
-!- FUNCTION: Single-stranded nucleic acid binding protein that binds
                                                                                                                                                                                                                                                                                                                                                           Kiledjian M., Wang X., Liebhaber S.A.;
"Identification of two KH domain proteins in the alpha-globin mRNP
stability complex.";
                                                                                                                                                     Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                           (Nucleic acid
                                                                                                                                                                                                                                MEDLINE=95331278; PubMed=7607214;
Leffers H., Dejgaard K., Celis J.E.;
"Characterisation of two major cellular poly(rC)-binding human proteins, each containing three K-homologous (KH) domains.";
Eur. J. Biochem. 230:447-453(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 601209; -. GO: C: Cytoplasm; NAS. GO: 00055737; C: Cytoplasm; NAS. GO: 00005634; C: Mucleus; NAS. GO: GO: 0003723; F: RNA binding; IDA. GO: 0003697; F: RNA binding; IDA. GO: 0000607; P: Single-stranded DNA binding; IDA. GO: 0016071; P: RNA metabolism; NAS.
           PCB1 HUMAN STANDARD; PRT; 356 AA.
013365; Q13157; Q14975;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
46-OCT-2001 (Rel. 40, Last annotation update)
Poly(rC) binding protein (Alpha-CP1) (hnRNP-E1)
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EMBL; U24223; AAA91317.1; -.
EMBL; 229505; CAA82631.1; ALT_FRAME.
HSSP; Q07244; IKHM.
Genew; HGNC:8647; PCBP1.
GK; Q15365; -.
MIM; 601209; -.
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=96016208; PubMed=7556077;
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InterPro; IPR004088; KH type 1.
Pfam; PF00013; KH; 3.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 14:4357-4364 (1995)
                                                                                                                                        sapiens (Human)
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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PCB1 HUMAN
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248 CAGTAIGTGGGTGCCATTATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 CATAAAGAGGCTAAGGACACCAAAACG-------GCTGACGAGGTTCCC 469
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|20 IlelysGluIleArgGluSerThrGlyAlaGlnValGlnValAlaGly-----AspMet
                                                                                                                                                                                                                                                                                                                                      188 GCGGGGCCCCCAGCCAAGCAGCAAGAGAAATCCCCCTTCGGCTCCTGGTGCCCACC
                                                                                                                                                                                                                                                                                                                                                                      3 AladlyValThrGluSerGlyLeuAsnValThrLeuThrlleArgLeuLeuMetHisGly
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SMART; SM00322; KH; 3.
PROSITE; PS50084; KH TYPE 1; 3.
Nuclear protein; RNA-binding; Ribonucleoprotein; DNA-binding;
Phosphorylation; Repeat.
DOMAIN
13 75 KH 1.
                                                               KH 1.

KH 2.

KH 3.

V -> A (IN REF. 2 AND 3).

V; DC85477576DC5104 CRC64;
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1138
71
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Matches:
Conservative:
Mismatches:
Indels:
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---AGCAGCGTTACTGGGGCTGCTCCC-----TATAGCTCCTTTATGCAGGCT 835

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Zhong R., Buckanovich R.J.,
                                                                                               MEDLINE=20182810; PubMed=10719891;
Jensen K.B., Dredge B.K., Stefani G., Zhong R., Buckanovich Okano H.J., Yang Y.Y.-L., Darmell R.B.;
Nova-1 regulates neuron-specific alternative splicing and essential for neuronal viability.";
Neuron 25:359-371(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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KH 2.
ALA-RICH.
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-!- SIMILARITY: Contains 3 KH domains.
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Nature 420:563-573(2002).
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SEQUENCE OF 250-493 FROM N.A.

REQUENCES STRAIN=C57BL/6J; TISSUB=Cerebellum;

RA MEDINIE=234683; PubMed=21466851;

RA MEDINIE=2334683; PubMed=21466851;

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Madari I.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Chocknia C., Corbanch J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Baldarelli R., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Madlett D.R., Matleais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea B.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sultana R., Mannayana-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Ranawa T., Pukuda S.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Rhiraki T., Waki K., Kawai J., Aizawa K., Arakwa T., Pukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Iloh M., Kagawa I.,

Ra Hara A., Hashizume W., Imotani K., Ishii Y., Iloh M., Kagawa I.,

Ra Khiraki T., Waki K., Sasaki D., Shibata K., Shinagawa J.,

Ra Khiraki T., Waki Y., Sigusi D., Shibata K., Shinagawa J.,

Rasunishi A., Yoshihoo W., Waterston R., Lander B.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                    956 CCACCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCC 1015
                                                                                                                                                                                                                                                                                        317 AsnPro---ValGluGlySerSerGlyArgGlnValThrIleThrGlySerAlaAlaSer 335
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1016 CAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTCAAGGAGGAGAACTTCTTTGGT 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 IleserLeuAlaGinTyrLeuIleAsnAlaArgLeuSerSerGluLysGlyMetGly 354
                                                                                                                                                                                                                                               AAGAAGGGGCAGCACCATCAAACAGCTCTCCCGGTTTGCCAGCGCGCTCCATCAAGATTGCA
                                                                                                       CCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCCCCCAGGCAGTGGGCGCCATCATCGGC
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MEDLINE=20458856; PubMed=11003693;
Ward-Bailey P.F., Wood B., Johnson K.R., Bronson R.T., Donahue L.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spontaneous mutation in the mouse.";
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"Neuromuscular ataxia: a new ;
Mamm. Genome 11:820-823(2000)
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SEQUENCE FROM N.A
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and so its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Dredge B.K., Darnell R.B.;
"Nova regulates GABA(A) receptor gamma2 alternative splicing via a "Nova regulates GABA(A) receptor gamma2 alternative splicing via a distal downstream UCAV-rich intronic splicing enhancer.";

Mol. Cell. Biol. 23:4687-4700(2003)
-!- FUNCTION: Punctions to regulate alternative splicing in neurons b binding pre-mRNA in a sequence-specific manner to activate exon inclusion. It binds specifically to the sequence UCAVY. Most likely acts to activate the inclusion of exon E3A in the glycine receptor alpha-2 chain and of exon E9 in gamma-aminobutyric-acid receptor gamma-2 subunit via a distal downstream UCAV-rich
                                                                                                                                                                                                                                                                                                                                                                   intronic splicing enhancer.
SUBCELLULAR LOCATION: Nuclear.
DISEASE: Defects in NOVAl leads to neuronal death in spinal and
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EMBL, AK047565; BAC33088.1; -.
MGJ, MGI.104297; NOVAI.; -.
GO; GO:0005634; C:nucleus; IC.
GO; GO:0003729; F:mRNA binding; IDA.
GO; GO:0006371; P:mRNA splicing; IDA.
InterPro; IPR004087; KH-dom.
Pfam; PF00013; KH; 3.
PRART; SM00322; KH; 3.
PROSITE; PS50084; KH-TYPE.1; 3.
Antiqen; Nuclear protein; RNA-binding; Repeat.
NON_TER
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Conservative:
Mismatches:
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NCBI_TaxID=9606;
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                                        ATTGGCAAGGAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGAC 325
                                                                                                                     GTGCATAGGAAGGAGAAC----GCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCC 379
                                                                                                                                                                                                    380 ACCCCTGAGGGCTGCTCCTCCGCT-----TGTAAGATGATCTTGGAGATTATG 427
                                                                                                                                                                                                                                -----GACACCAAAACGGCTGACGAGTT 466
                                                                                                                                                                                                                                                                                                                                                                                                     131 AspArgIleLysGlnThrLeuProSerSerProThrThrThrLysSerSerProSerAsp 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||:::
|ProMetThrThrSerArgAlaAsnGlnValLysIleIleValProAsnSerThrAlaGly 170
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                                                                                                                                                            LeuSerLysSerLysAspPheTyrProGlyThrThrGluArgValCysLeuIleGlnGly 90
                                                                  ||||||||| ||| ||| |||||| ::: ||||:::||| ::: |||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: ||| ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || :: || ::: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: ||
GlyGluAspGlyGlnTyrPheLeuLysValLeuIleProSerTyrAlaAlaGlySerIle
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1183
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                                                                     383 GlyTyrPheGlyAlaAlaSerProLeuAlaAlaSerAlaIleLeuGlyThrGluLysSer 402
                                                                                                                                                                                                                                                                                                                                      AlaArgIleGlnIleSerLysLysGlyGluPheValProGlyThrArgAsnArgLys--- 457
                                                                                                                                                                                              ||| |||||| :::
403 ThrAspGlySerLysAspValValGlu------IleAlaValProGlùAsnLeu
                                                                                                                                                                                                                                                                                               1124 GCTGGCCGGGTCATTGGCAAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCA
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"Nova, the paraneoplastic Ri antigen, is homologous to an RNA-binding
protein and is specifically expressed in the developing motor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
RNA-Dinding protein Nova-1 (Neuro-oncological ventral antigen 1)
(Onconeural ventral antigen-1) (Paraneoplastic Ri antigen) (Ventral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structure 7:191-203 (1999).
-!- FUNCTION: May regulate RNA splicing or metabolism in a specific subset of developing neurons.
-!- SUBCELUMAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isold=P51513-3; Sequence=VSP_002842;
TISSUE SPECIFICITY: Brain.
DISEASE: Autoantigen in the paraneoplastic opsoclonus myoclonus
ataxia (POWA), a paraneoplastic neurological syndrome/disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSP_002843, VSP_002844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99148126; PubMed=10368286;
Lewis H.A., Chen H., Edo C., Buckanovich R.J., Yang Y.Y.-L.,,
Musunuru K., Zhong R., Darnell R.B., Burley S.K.,
"Crystal structures of Nova-1 and Nova-2 K-homology RNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUBE-Fetal brain;
Dmitrenko V.V., Garifulin O.M., Shostak K.A., Smikodub A.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1238 GTGAAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAA 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
1013 GCCCAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 423-495.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Cerebellum, and Hippocampus;
MEDLINE-94000830; PubMed-8398153;
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1016 CAATTCAAGGCTCAGGGAAGAATCTATGGCAAACTC-----AAGGAGGAGAACTTC 1066
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                                                                                                                                                                                   AsnValAlaLysThrGluProValSerIleLeuGlnProGlnThrThrValAsnProAsp 148
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                                                                                 TGTAAGATGATCTTGGAGATTATGCAT 430
                                                                                                                ValdiuAlaLeuAsnAlaValHisGlyPheIleAlaGluLysileArgGluMetProGln 128
              ---GGTGCAGCTGAAAAGCCATCAGTGTGCACTCCACC 382
                                       :::
||| SerLysSerLysAspPheTyrProGlyThrThrGluArgValCysLeuIleGlnGlyThr
                                                                                                                                                                                                                                                                                                                  169 MetThrThrSerArgAlaAsnGlnValLysIleileValProAsnSerThrAlaGlyLeu
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328 TyrGlyTyrAsnLeuAsnThrLeuGlyLeuGlyLeuSerGlnAlaAlaAlaThrGlyAla
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                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB. Outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ATCCCCCTTCGGCTCCTGGTGCCCAACTATGTGGGTGCCATTATTGGCAAGGAG 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PNS/D) associated with breast cancer, fallopian cancer, and SCLCa and characterized primarily by loss of inhibitory control of motor neurons in the spinal cord and brainstem. Recognized by the IgG autoantibody ANNA-2 (also called anti-Ri). SIMILARITY: Contains 3 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 GlnAsnGlyThrHisThrGlyValProIleAspLeuAspProProAspSerArgLysArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00013; KH; 3. SMART; SM00322; KH; 3. PROSITE; PS50084; KH_TYPE_1; 3. Antigen; Nuclear protein; RNA-binding; Repeat; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEAR LOCALIZATION SIGNAL
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Missing (in isoform 3).
/FTIG=VSP_002842.
/VIIDENS -> FTIG=VSP_002843.
/FTIG=VSP_002843.
/FTIG=VSP_002844.
/FTIG=VSP_002844.
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KH 2.
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KH 3.
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Matches:
Conservative:
Mismatches:
Indels:
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GO:0007626; P:locomotory behavior; TAS.
GO:0008380; P:RNA splicing; TAS.
GO:0007268; P:synaptic transmission; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-270-437D-5 (1-1708) x NOA1_HUMAN (1-510)
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InterPro; IPR004088; KH_type_1.
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GK; P51513; -.
MIM; 602157; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                             475
                      ||| |||::: |||:::
|AspGlySerLysAspValValGlu------IleAlaValProGluAsnLeuVal
                                                                               GGCCGGGTCATTGGCAAAGGTGGAAAAACGGTGAACGAGTTGCAGAATTTGACGGCAGCT
                                                                                                                                                   SEQUENCE FROM N.A.
MEDILINE-92507122; PubMed-10101190;
MEDILINE-92507122; PubMed-10101190;
Thiele B.J., Berger M., Huth A., Reimann I., Schwarz K., Thiele H.;
Triele B.J., Berger M., Huth A., Reimann I., Schwarz K., Thiele H.;
Triesue-specific translational regulation of alternative rabbit
15-lipoxygenase mRNNs differing in their 3'-untranslated regions.";
Nucleic Acids Res. 27:1828-1836(1999).
-i. FUNCTION: Single-stranded nucleic acid binding protein that binds
preferentially to oligo ac (By similarity).
-i. SUBCELLULAR LOCATION: Nuclear (By similarity).
-i. SIMILARITY: Contains 3 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                          1241 AAAATCATCGGACATTTCTATGCCAGTCAGATGGCTCAA 1279
                                                                                                                                                                                                               ThrileThrGlyThrProAlaAlaThrGlnAlaAlaGln 488
                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1).
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(Rel. 40, Last sequ
(Rel. 40, Last anno
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16-OCT-2001
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CCCGAAACACCTGACTCCAAAGTTCGTATGGTTATCATCACTGGACCGCCAGAGGCCCAA 1018
                                                                                            CAGTATGTGGGGTGCCATTATTGGCAAGGAGGGCCACCATCCGCAACATCACAAAACAG 307
                                                                                                                                                                                                                    308 ACCCAGTCCAAGATAGACGTGCATAGGAAGGAGAACGCAGGTGCAGCTGAAAAAGCCATC 367
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SerGlyAlaArgIleAsnIle-----SerGluGlyAsnCysProGluArgIleIle 59
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| GluGluAspIleAsnSerSerMetThrAsnSerThrAlaAlaSerArgProProValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 LeuargLeuValValProAlaThrGlnCysGlySerLeuIleGlyLysGlyGlyCysLys
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| 178 ValMetThrIleProTyrGlnProMetProAlaSerSerProValIleCysAlaGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           590 ACCCTTTACAACCCTGAGAGGACCATCACTGTGAAGGGGGCCATCGAGAATTGTTGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 LeuAsnGlnValAlaArgGlnGlnSerHisPheAlaMetMetHisGlyGlyThrGlyPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428 CATAAAGAGGTAAGGACACCAAAACG-----
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US-09-270-437D-5 (1-1708) x PCB1\_RABIT (1-356)

356 75 75 69 9

Conservative: Mismatches:

9.26e-07 218.50 41.90% 20.95% 7.03%

Similarity: cal Similarity:

No.:

Best Local S Query Match:

Indels:

Gaps:

Length: Matches:

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MEDINE-2238257; PubMed=12477932;

MEDINE-2238257; PubMed=12477932;

MEDINE-2238257; PubMed=12477932;

MAISCHIL S.P., Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Mala S.S., Loquellano N.A., Feters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci D., Mullahy S.J.,

Raha S.S., Morbay K.C., Male S., Garrinci D., Mullahy S.J.,

Bosak S.A., McKernan K.J., Malek J.A., Gubbs R.A.,

Willalon D.K., Muzzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y. Schein J.B., Jones S.J.M., Marra M.A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield X. Schein J.B., Jones S.J.M., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length

From Matl. Acad. Sci. US.A. 99:16899-16903(2002).

Proferentially to oligo do (By similarity).

SIMILARITY: Contains 3 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
ISOGAI T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninoniya K., Iwayanagi T.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20396135; PubMed=10936052; Makeyev A.V., Liebhaber S.A.; "Identification of two novel mammalian genes establishes a subfamily of KH-domain RNA-binding proteins."; Genomics 67:301-316 (2000).
                                                                                                                                                                                                                          Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
Poly(rC)-binding protein 4 (Alpha-CP4).
  403 AA
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GO; GO:0005634; C:nucleus; ISS.
GO; GO:0003677; F:DNA binding; ISS.
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EMBL, AK02393; BAB14761.1; -.
EMBL, BC003008, AAH03008.1; -.
EMBL, BC004153; AAH04153.1; -.
  STANDARD;
                                                                                                                                                                                                  Homo sapiens (Human)
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SEQUENCE FROM N.A.
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198 GlyPheSerValGlnGlyGlnTyrGlyAlaValThrProAlaGluValThrLysLeuGln 217
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GO; GO:0016071; P:RNA metabolism; ISS.
InterPro; IPR004088; KH-dym.
InterPro; IPR004188; KH-type-1.
Pfam; PF00013; KH; 3.
SMART; SM00322; KH; 3.
PROSITE; PSS0094; KH TYPE 1; 3.
Nuclear protein; RNA-binding; Ribonucleoprotein; DNA-binding;
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215 GTGGACAICCCCCTICGGCTCCTGGTGCCCACCCAGTAIGTGGGTGCCATTAITGGCAAG 274
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                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                          GCAGTGGGCGCCATCATCGGCAAGAAGGGGCAGCACATCAAACAGCTCTCCCGGTTTGCC 934
                                                                       AGCGCCTCCATCAAGATTGCACCACCCGAAACACCTGACTCCAAAGTTCGTATGGTTATC 994
                                                                                                                                                                                                                                                                                                                                                                    acid binding protein that binds
                                                                                                                                                                                                                                                                                                                MEDLINE=20396135; PubMed=10936052;
Makeyev A.V., Liebhaber S.A.;
"Identification of two novel mammalian genes establishes a subfamily
of KH-domain RNA-binding proteins.";
Genomics 67:301-316(2000).
                                                                                                                                                                                                                                                              Craniata, Vertebrata, Buteleostomi,
Sciurognathi, Muridae, Murinae, Mus
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115
65
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-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: Contains 3 KH domains.
                                                                                                               995 ATCACTGGACCGCCAGAGGCCCAATTCAAGGCTCAG 1030
                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly(rC)-binding protein 4 (Alpha-CP4).
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M M M 3.5.1
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InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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403 AA;
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JS-09-270-437D-5 (1-1708) x PCB4\_MOUSE (1-403)

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GAGGGGCCACCATCCGCAACATCACAAAACAGACCCAGTCCAAGATAGACGTGCATAGG 334
                                                                                                                                                          335 AAGGAGAACGCAGGTGCAGCTGAAAAAGCCATCAGTGTGCACTCCACCCCTGAGGGCTGC 394
                                                                                                                                                                                                                                                                                                                                                                                                 83 LeuAspGluAspLeuCysAlaAlaProAlaAsnGlyGlySerValSerArgProProVal 102
                                                                                                                                                                                                                                                                                                                                                                                                                                               AACCTGAAGAAGGTAGAGCAAGATACCGAGACAAAAATCACCATCTCCTCGTTGCAAGAC 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         647 AGGGCCGAGCAGGAAATAATGAAGAAGTTCGGGAGGCCTATGAGAATGATGTGGCTGCC 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  814
                                                                                                                                                                                                                                                      395 TCCTCCGCTTGTAAGATGATCTTGGAGATTATGCATAAAGAGGCTAAGGGACACCAAAACG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 TATAGCTCCTTTATGCAGGCTCCCGAGCAGGAGATGGTGCAGGTGTTTATCCCCGCCCAG 874
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52 -------sprogluargile 62
                                                                                                                                                                                                                                                                                              ThrThrIleThrGlySerThrAlaAlaValPheHisAlaValSerMetIleAlaPheLys 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              764 -----TCATCCAGCGCAGTCCCG---CCGCCTCCCAGCAGCGTTACTGGGGCTGCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 GCAGTGGGCGCCATCATCGGCAAGAGGGGCAGCACATCAAACAGCTCTCCCGGTTTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAGCTCTCACCTGATCCCTGGCCTGAACCTGGCTGCTA--------
                                                                                                          36 LysGlyGluThrValLysArgileArgGluGlnSerSerAlaArgile-----
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                                                                                                                                                                                                                                                                                                                                                   455 GCTGACGAG-----
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
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                                                                                                                                                                                                                                                                                                                                                                                                                                           erroneous
                                                                                                                                                                                                                                                                              Isoid=P58223-2; Sequence=VSP_008899, VSP_008900;
Note=May be due to a competing acceptor site. No experimental
confirmation available;
SIMILARITY: Contains 5 KH domains.
GAUTION: Ref.1 sequences differ from that shown due to erroneous
gene model prediction. At4g18370 and At4g18375 were originally
fused into a single gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R EMBL, AL021710; CAA16717.1; ALT SEQ.
R EMBL, AL161548; CAA78839.1; ALT SEQ.
R EMBL, AX133701; AAM91635.1; -...
R EMBL; BY00108; AAM64172.1; -...
R InterPro; IPR004089; KH_type_1.
R Dfan; PP000131; KH; 5...
R PROSITE; PS50094; KH TYPE 1; 5...
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/FIIdavSP 008899.
Missing (In isoform 2).
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w; 61F135BB8647C0C CRC64;
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105
91
201
124
22
                                                                                                                                                                                IsoId=P58223-1; Sequence=Displayed;
Note=No experimental confirmation available;
                       -!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
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Matches:
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Mismatches:
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533	514 PheProAlaGlyAspAsnValLeuGlySerThrGlyProTyrSerTyrGlyArgLeuPro 533	514	QC
1492	1433 AGGCCTGAGAATGAGAGGGAATCCGGGAACACNTGGGCCGGGCTGTAGATCAGGTTTGCCC 1492		ò
513	494 ThrieuProSerPheMetSerSerMetAlaSerThrSerGlyPheHisGlyTyrGlySer 513	494	QQ
1432	1421 GCTCTCCCCGGC 1432	1421	ò
493	475ProProAlaArgThrAspAsnCysSerPheLeuSerGlySerSerAsnAlaGlyTyr 493	475	Ω
1420	1367 GCCCCTCCCTGTCCCTINGAGTCCAGGACAACAACGGGCAGAAATCGAGAGTGT 1420	1367	ò
474	458 ArgLeuArgGluAspValLeuGlyAspLysAspSerValAlaThrArgLys 474	458	DP DP